

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2006, 22:56:42 ; Search time 2483 Seconds  
(without alignments)

360.557 Million cell updates/sec

Title: US-10-824-036A-3578

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ACCESSION CQ967218  
VERSION CQ967218.1 GI:5614984  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Mcswiggen, J., Beigelman, L., Uman, N., Haerberli, P., Chowrira, B. and Polisky, B.  
TITLE RNA interference mediated inhibition of MAP kinase gene expression using short interfering nucleic acid (siNA)  
JOURNAL Patent: WO 2004097(20-A 1858 11-NOV-2004;  
Sirma Therapeutics, Inc (US)  
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ACCESSION CQ974653  
VERSION CQ974653.1 (..57998833)

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REFERENCE   1
AUTHORS     McSwiggen,J. and Chowrira,B.
TITLE       RNA interference mediated inhibition of platelet-derived
            endothelial cell growth factor (ECGF1) gene expression using short
            interfering nucleic acid (siNA)
JOURNAL     Patent: WO 2004111237-A 258 23-DEC-2004;
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ACCESSION CQ989002
VERSION   CQ989002.1 GI:58196690
KEYWORDS  synthetic construct
SOURCE    synthetic construct
ORGANISM  other sequences; artificial sequences.
REFERENCE 1
AUTHORS   McSwiggen,J. and Beigelman,L.
TITLE     RNA interference mediated treatment of Alzheimer's disease using
            short interfering Nucleic Acid (siNA)
JOURNAL   Patent: WO 2005003350-A 1901 13-JAN-2005;
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ACCESSION CQ910063
VERSION   CQ910063.1 GI:59669892
KEYWORDS  synthetic construct
SOURCE    synthetic construct
ORGANISM  other sequences; artificial sequences.

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AUTHORS     Uman,N. and McSwiggen,J.
TITLE       RNA interference mediated inhibition of B7-H1 gene expression using
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JOURNAL     Patent: WO 2005007855-A 295 27-JAN-2005;
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ACCESSION CS015515
VERSION   CS015515.1 GI:59675319
KEYWORDS  synthetic construct
SOURCE    synthetic construct
ORGANISM  other sequences; artificial sequences.
REFERENCE 1
AUTHORS   McSwiggen,J. and Uman,N.
TITLE     RNA interference mediated inhibition of acetyl-coa-carboxylase gene
            expression using short interfering nucleic acid (siNA)
JOURNAL   Patent: WO 2005007859-A 952 27-JAN-2005;
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VERSION   CS028804.1 GI:60498345
KEYWORDS  synthetic construct
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ORGANISM  other sequences; artificial sequences.
REFERENCE 1
AUTHORS   McSwiggen,J. and Chowrira,B.M.
TITLE     RNA interference mediated inhibition of XIAP gene expression using
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JOURNAL   Patent: WO 2005014811-A 1057 17-FEB-2005;

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DEFINITION
Sequence 2028 from Patent WO2005028650.
ACCESSION
CS091306
VERSION
CS091306.1 GI:66716563
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
synthetic construct; artificial sequences.
REFERENCE
1 Jadhav,V., Kossen,K., Zinnen,S., Vaish,N. and Mcswiggen,J.
AUTHORS RNA interference mediated inhibition of Hepatitis C Virus (HCV)
TITLE expression using short interfering Nucleic Acid (siNA)
JOURNAL Patent: WO 2005028650-A 2028 31-MAR-2005;
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DEFINITION
Sequence 371 from Patent WO2005045034.
ACCESSION
CS091762
VERSION
CS091762.1 GI:66949338
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
synthetic construct; artificial sequences.
REFERENCE
1 Mcswiggen,J., Haerberli,P. and Beigelman,L.
AUTHORS RNA interference mediated treatment of Parkinson disease using
TITLE short interfering Nucleic Acid (siNA)
JOURNAL Patent: WO 2005045034-A 371 19-MAY-2005;
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DEFINITION
Sequence 471 from Patent WO2005045032.
ACCESSION
CS092397
VERSION
CS092397.1 GI:66949935
KEYWORDS
synthetic construct
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synthetic construct
ORGANISM
synthetic construct; artificial sequences.
REFERENCE
1 Usman,N. and McSWIGGEN,J.
AUTHORS RNA interference mediated inhibition of early growth response gene
TITLE expression using short interfering Nucleic Acid (siNA)
JOURNAL Patent: WO 2005045032-A 471 19-MAY-2005;
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DEFINITION
Sequence 455 from Patent WO2005045039.
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VERSION
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KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
synthetic construct; artificial sequences.
REFERENCE
1 Richards,I., and McSWIGGEN,J.
AUTHORS RNA interference mediated inhibition of intercellular adhesion
TITLE molecule (ICA) gene expression using short interfering Nucleic
JOURNAL Acid (siNA)
Patent: WO 2005045039-A 455 19-MAY-2005;
Sirna Therapeutics, Inc. (US)
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ACCESSION CS094005  
VERSION CS094005.1 GI:66951519  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Mcswiggen,J. and Polisky,B.  
TITLE RNA interference mediated inhibition of hairless (hr) gene  
expression using short interfering nucleic acid (siRNA)  
JOURNAL Patent: WO 2005045036-A 1139 19-MAY-2005;  
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ACCESSION CS094006  
VERSION CS094006.1 GI:66951520  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Mcswiggen,J.  
TITLE RNA interference mediated inhibition of hairless (hr) gene  
expression using short interfering nucleic acid (siRNA)  
JOURNAL Patent: WO 2005045036-A 1140 19-MAY-2005;  
SiRNA Therapeutics, Inc. (US)  
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ACCESSION CS094331  
VERSION CS094331.1 GI:66951836  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Mcswiggen,J. and Polisky,B.  
TITLE RNA interference mediated inhibition of cholesterol ester transfer  
protein (cetp) gene expression using short interfering nucleic acid  
(siRNA)  
JOURNAL Patent: WO 2005045041-A 323 19-MAY-2005;  
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ACCESSION CS095629  
VERSION CS095629.1 GI:66952207  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Mcswiggen,J., Chowrira,B.M. and Haerberli,P.  
TITLE RNA interference mediated inhibition of NOGO and NOGO receptor gene  
expression using short interfering Nucleic Acid (siNA)  
JOURNAL Patent: WO 2005045035-A 321 19-MAY-2005;  
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KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS McSwiggen,J., Chowira,B.M. and Haerberli,P.
TITLE RNA interference mediated inhibition of Nogo and Nogo receptor gene
expression using short interfering Nucleic Acid (siNA)
JOURNAL Patent: WO 2005045035-A 322 19-MAY-2005;
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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	40	14	100.0	14	AEBO9186	Target se
	41	14	100.0	14	AEBO9186	Target se
	42	14	100.0	14	AEBO9186	Human tel
	43	14	100.0	14	AEBO9186	Human MDR
c	44	14	100.0	14	AEBO9186	Novel hum
	45	14	100.0	14	AEBO9186	Target-co
		14	100.0	14	AEBO9186	Target se

ALIGNMENTS

RESULT 1  
ADT66481  
ID ADT66481 standard; RNA; 14 BP.  
AC ADT66481;  
XX  
XX  
XX  
13-JAN-2005 (first entry)  
Target sequence containing 5' palindrome/repeat.  
siRNA; short interfering RNA; ss; RNA interference; gene silencing.  
Synthetic.  
WO2004092383-A2.  
28-OCT-2004.  
13-APR-2004; 2004WO-US011320.  
15-APR-2003; 2003US-0462874P.  
30-APR-2003; 2003US-00427160.  
23-MAY-2003; 2003US-00444853.  
23-OCT-2003; 2003US-00693059.  
24-NOV-2003; 2003US-00720448.  
14-JAN-2004; 2004US-00757803.  
(SIRN-) SIRNA THERAPEUTICS INC.  
Mcswiggen J, Bharat C, Haerberli P;  
WPI; 2004-766879/75.  
Novel chemically synthesized double stranded short interfering nucleic acid molecule directing cleavage of severe acute respiratory syndrome virus RNA through RNA interference, useful for treating viral infection.  
Disclosure; Fig 14; 219pp; English.  
The invention relates to a chemically synthesised double stranded short interfering ribonucleic acid (siRNA) molecule directing cleavage of

CC severe acute respiratory syndrome (SARS) virus RNA through RNA  
CC interference, comprising a strand having nucleotide sequence with  
CC sufficient complementarity to the SARS virus RNA to direct cleavage of  
CC the SARS virus RNA through RNA interference, where the siRNA does not  
CC require the presence of nucleotides having a 2'-hydroxy group for  
CC mediating RNA interference, and each strand of is 19-23 nucleotides in  
CC length. The siRNA is useful for modulating the expression of genes of  
CC associated with the development or maintenance of SARS virus infection,  
CC acute respiratory failure, viral pneumonia and/or disease states  
CC associated with SARS virus infection, and for treating SARS virus  
CC infection, acute respiratory failure, viral pneumonia and/or disease  
CC states associated with SARS virus infection by preventing the  
CC transcription of SARS gene. The siRNA is useful in diagnosis, and  
CC treatment of diseases and conditions that respond to the modulation of  
CC SARS virus gene expression and/or activity. The siRNA is useful in  
CC therapeutic, diagnostic, target validation, genomic discovery, genetic  
CC engineering, and pharmacogenomic applications. The siRNA is stable and  
CC capable of mediating RNA interference against SARS inside a cell or  
CC reconstituted in vitro system, and has high degree of specificity with  
CC respect to SARS RNA expression. The present sequence is sequence used to  
CC illustrate the principle of designing siRNA molecules based on  
CC palindromic or repeat containing target sequences.

XX SQ Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 14; DB 13; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUCUAUUUCG 14  
|||||  
DB 1 AUAUAUCUAUUUCG 14

RESULT 2  
ADU66346  
ID ADU66346 standard; RNA; 14 BP.  
XX AC ADU66346;  
XX  
DT 27-JAN-2005 (first entry)  
XX  
DE Palindrome utilizing duplex oligonucleotide exemplary sequence #1.  
XX  
KW RNA interference; mitogen activated protein kinase inhibitor;  
KW inflammation; immunosuppressive; immune disorder; autoimmune disease;  
KW allergy; antiallergic; cytostatic; neoplasm; cancer; ss.  
XX  
OS Synthetic.  
XX  
PN WO2004097020-A2.  
XX  
PD 11-NOV-2004.  
XX  
PF 23-APR-2004; 2004WO-US012517.  
XX  
PR 25-APR-2003; 2003US-00424339.  
PR 30-APR-2003; 2003US-00427160.  
PR 23-MAY-2003; 2003US-00444853.  
PR 23-OCT-2003; 2003US-00693059.  
PR 24-NOV-2003; 2003US-00720448.  
PR 14-JAN-2004; 2004US-00757803.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswiggen J, Beigelman L, Usman N, Haerberli P, Chowrira B;  
PI Polisky B;  
XX  
DR WPI; 2005-012649/01.  
XX  
PT Novel short interfering nucleic acid molecule useful for inhibiting  
PT mitogen activated protein kinase gene expression e.g., c-JUN associated  
PT with diseases e.g., inflammatory disease or autoimmune disease.

XX Disclosure; SEQ ID NO 1858; 322pp; English.  
XX  
CC The invention relates to a chemically synthesized double stranded short  
CC interfering nucleic acid (siRNA) molecule (I) that directs cleavage of a c  
CC -JUN RNA through RNA interference (RNAi), where one strand of the siRNA  
CC molecule comprises nucleotide sequence having sufficient complementarity  
CC to the c-JUN RNA for the siRNA molecule to direct cleavage of the c-JUN  
CC RNA through RNA interference. (I) is useful for inhibiting mitogen  
CC activated protein kinase gene (e.g., c-JUN, JNK1, JNK2, p38, ERK1 or  
CC ERK2) expression associated with diseases e.g., inflammatory disease,  
CC autoimmune disease, allergy, cancer. (I) exhibits improved RNA  
CC interference activity and nuclease resistance. The present sequence  
CC represents a palindrome utilizing duplex oligonucleotide exemplary  
CC sequence.

XX SQ Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 14; DB 14; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUCUAUUUCG 14  
|||||  
DB 1 AUAUAUCUAUUUCG 14

RESULT 3  
ADV60863  
ID ADV60863 standard; RNA; 14 BP.  
XX AC ADV60863;  
XX  
DT 10-MAR-2005 (first entry)  
XX  
DE Duplex forming oligonucleotide, target sequence.  
XX  
KW ss; gene silencing; siRNA; short interfering RNA; RNA interference;  
KW DNA-RNA hybrid.  
XX  
OS Synthetic.  
XX  
PN WO2004111237-A1.  
XX  
PD 23-DEC-2004.  
XX  
PF 16-APR-2004; 2004WO-US011848.  
XX  
PR 16-APR-2003; 2003US-00417012.  
PR 24-APR-2003; 2003US-00422704.  
PR 30-APR-2003; 2003US-00427160.  
PR 23-MAY-2003; 2003US-00444853.  
PR 29-AUG-2003; 2003US-00652791.  
PR 23-OCT-2003; 2003US-00693059.  
PR 24-NOV-2003; 2003US-00720448.  
PR 14-JAN-2004; 2004US-00757803.  
PR 13-FEB-2004; 2004US-00780447.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswiggen J, Chowrira B;  
XX  
DR WPI; 2005-040107/04.  
XX  
PT New chemically synthesized double stranded short interfering ribonucleic  
PT acid (siRNA), useful in preparing a composition for inhibiting platelet-  
PT derived endothelial cell growth factor (ECFG1) gene expression for  
PT treating e.g., cancer.  
XX  
PS Disclosure; Fig 14; 197pp; English.  
XX  
CC The invention relates to a new chemically synthesized double stranded  
CC short interfering ribonucleic acid (siRNA) molecule directs cleavage of a



CC platelet-derived endothelial cell growth factor (ECGF1) RNA via RNA  
 CC interference (RNAi). Also included is a composition comprising the siRNA  
 CC molecule in a carrier or diluent. The siRNA molecule is useful in  
 CC preparing a composition for inhibiting platelet-derived endothelial cell  
 CC growth factor (ECGF1) gene expression for treating proliferative diseases  
 CC e.g., cancers, lymphomas, carcinomas, sarcomas, tumor angiogenesis,  
 CC macular degeneration, corneal neovascularization, diabetic retinopathy,  
 CC neovascular glaucoma, myopic degeneration, restenosis and polycystic  
 CC kidney disease. The present sequence is a sequence used to illustrate  
 CC duplex forming oligonucleotides which incorporate a palindromic or repeat  
 CC sequence and their use as siRNAs.

SQ Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;  
 Query Match 100.0%; Score 14; DB 14; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUAUAUCUAUUUCG 14  
 Db 1 AUAUAUCUAUUUCG 14

RESULT 4  
 ADW28003  
 ID ADW28003 standard; RNA; 14 BP.  
 AC ADW28003;  
 XX  
 XX 07-APR-2005 (first entry)  
 DE Cholinergic receptor muscarinic 3 gene targeted siRNA #300.  
 XX  
 KW gene expression; antiasthmatic; antiallergic; antiinflammatory; CNS-Gen.;  
 KW respiratory-gen.; hypotensive; gastrointestinal-gen.; neuroprotective;  
 KW neotropic; uropathic; short interfering RNA; RNA interference; siRNA;  
 KW cholinergic receptor muscarinic 3; asthma; allergic rhinitis; sinusitis;  
 KW inflammation; allergy; cystic fibrosis; pulmonary vasoconstriction;  
 KW hypertension; emphysema; irritable bowel syndrome; Alzheimers disease;  
 KW incontinence; ss.  
 XX  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH misc\_difference 13..14  
 FT /\*tag= a  
 FT /note= "deoxythymidine nucleotide"  
 PN US2005014172-A1.  
 XX  
 PD 20-JAN-2005.  
 XX  
 XX 11-MAR-2004; 2004US-00798090.  
 XX  
 XX 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 20-MAY-2002; 2002WO-US015876.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0409293P.  
 PR 09-SEP-2002; 2002US-040129P.  
 PR 15-JAN-2003; 2003US-US005028.  
 PR 20-FEB-2003; 2003WO-US005346.  
 PR 30-APR-2003; 2003US-00427160.  
 PR 23-MAY-2003; 2003US-0044853.  
 PR 23-OCT-2003; 2003US-00693059.  
 PR 24-NOV-2003; 2003US-00720448.  
 PR 14-JAN-2004; 2004US-00757803.  
 XX  
 XX (RICH/) RICHARDS I.  
 PA (MCSW/) MCSWIGGEN J.  
 XX

PI Richards I, Mcswiggen J;  
 XX WPI; 2005-090672/10.  
 XX  
 XX Novel chemically synthesized double stranded short interfering nucleic  
 PT acid molecule that directs cleavage of cholinergic receptor muscarinic 3  
 PT RNA through RNA interference, useful for treating asthma.  
 XX  
 XX Disclosure; SEQ ID NO 309; 84pp; English.  
 XX  
 CC The invention relates to a chemically synthesized double stranded short  
 CC interfering nucleic acid (siNA) molecule (I) that directs cleavage of a  
 CC cholinergic receptor muscarinic 3 (CHRM3) RNA through RNA interference,  
 CC where each strand of (I) has 19-23 nucleotides, and does not require the  
 CC presence of nucleotides having a 2-hydroxy group for mediating RNA  
 CC interference. (I) is useful for treating diseases e.g., asthma, allergic  
 CC rhinitis, sinusitis, inflammation, allergy, cystic fibrosis, pulmonary  
 CC vasoconstriction or hypertension, emphysema, irritable bowel syndrome,  
 CC Alzheimer's disease or urinary incontinence. (I) has increased resistance  
 CC towards nuclease. Double stranded short interfering nucleic acid molecule  
 CC was produced by solid phase oligonucleotide synthesis method. This  
 CC sequence represents an example of a siRNA molecule of the invention.

SQ Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;  
 Query Match 100.0%; Score 14; DB 14; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUAUAUCUAUUUCG 14  
 Db 1 AUAUAUCUAUUUCG 14

RESULT 5  
 ADW27999  
 ID ADW27999 standard; RNA; 14 BP.  
 XX  
 AC ADW27999;  
 XX  
 XX 07-APR-2005 (first entry)  
 XX  
 DE Cholinergic receptor muscarinic 3 gene targeted siRNA #296.  
 XX  
 KW gene expression; antiasthmatic; antiallergic; antiinflammatory; CNS-Gen.;  
 KW respiratory-gen.; hypotensive; gastrointestinal-gen.; neuroprotective;  
 KW neotropic; uropathic; short interfering RNA; RNA interference; siRNA;  
 KW cholinergic receptor muscarinic 3; asthma; allergic rhinitis; sinusitis;  
 KW inflammation; allergy; cystic fibrosis; pulmonary vasoconstriction;  
 KW hypertension; emphysema; irritable bowel syndrome; Alzheimers disease;  
 KW incontinence; ss.  
 XX  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH misc\_difference 13..14  
 FT /\*tag= a  
 FT /note= "deoxythymidine nucleotide"  
 PN US2005014172-A1.  
 XX  
 PD 20-JAN-2005.  
 XX  
 XX 11-MAR-2004; 2004US-00798090.  
 XX  
 XX 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 20-MAY-2002; 2002WO-US015876.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0409293P.  
 PR 09-SEP-2002; 2002US-0408378P.  
 PR 15-JAN-2003; 2003US-00720448.  
 PR 14-JAN-2004; 2004US-00757803.  
 XX  
 XX (RICH/) RICHARDS I.  
 PA (MCSW/) MCSWIGGEN J.  
 XX

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PR 20-FEB-2003; 2003WO-US005028.
PR 20-FEB-2003; 2003WO-US005346.
PR 30-APR-2003; 2003US-00427160.
PR 23-MAY-2003; 2003US-00444853.
PR 23-OCT-2003; 2003US-00693059.
PR 24-NOV-2003; 2003US-00720448.
PR 14-JAN-2004; 2004US-00757803.
XX
PA (RICH/) RICHARDS I.
PA (MCSW/) MCSWIGGEN J.
XX
PI Richards I, Mcswiggen J;
XX
XX WPI; 2005-090672/10.
XX
XX Novel chemically synthesized double stranded short interfering nucleic
PT acid molecule that directs cleavage of cholinergic receptor muscarinic 3
PT RNA through RNA interference, useful for treating asthma.
XX
XX Disclosure; SEQ ID NO 305; 84pp; English.
XX
XX The invention relates to a chemically synthesized double stranded short
CC interfering nucleic acid (siNA) molecule (I) that directs cleavage of a
CC cholinergic receptor muscarinic 3 (CHRM3) RNA through RNA interference,
CC where each strand of (I) has 19-23 nucleotides, and does not require the
CC presence of nucleotides having a 2-hydroxy group for mediating RNA
CC interference. (I) is useful for treating diseases e.g., asthma, allergic
CC rhinitis, sinusitis, inflammation, allergy, cystic fibrosis, pulmonary
CC vasoconstriction or hypertension, emphysema, irritable bowel syndrome,
CC Alzheimer's disease or urinary incontinence. (I) has increased resistance
CC towards nuclease. Double stranded short interfering nucleic acid molecule
CC was produced by solid phase oligonucleotide synthesis method. This
CC sequence represents an example of a siRNA molecule of the invention.
XX
XX Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;
XX
XX Query Match 100.0%; Score 14; DB 14; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+03;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 AUAUAUCUAUUUCG 14
Db 1 AUAUAUCUAUUUCG 14
XX
XX RESULT 6
XX ADW28009
XX ID ADW28009 standard; RNA; 14 BP.
XX AC ADW28009;
XX
XX 07-APR-2005 (first entry)
XX
XX Cholinergic receptor muscarinic 3 gene targeted siRNA #306.
XX
XX gene expression; antiasthmatic; antiallergic; antiinflammatory; CNS-Gen.;
XX respiratory-gen.; hypotensive; gastrointestinal-gen.; neuroprotective;
XX neurotropic; uropathic; short interfering RNA; RNA interference; siRNA;
XX cholinergic receptor muscarinic 3; asthma; allergic rhinitis; sinusitis;
XX inflammation; allergy; cystic fibrosis; pulmonary vasoconstriction;
XX hypertension; emphysema; irritable bowel syndrome; Alzheimers disease;
XX incontinence; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH misc_difference 13..14
XX FT /*tag= a
XX FT /note= "deoxythymidine nucleotide"
XX
XX US2005014172-A1.
XX
XX 20-JAN-2005.
XX

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XX 11-MAR-2004; 2004US-00798090.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 20-MAY-2002; 2002WO-US015876.
XX 06-JUN-2002; 2002US-0386782P.
XX 29-AUG-2002; 2002US-0406784P.
XX 09-SEP-2002; 2002US-0408378P.
XX 15-JAN-2003; 2003US-0409293P.
XX 20-FEB-2003; 2003WO-US005028.
XX 20-FEB-2003; 2003WO-US005346.
XX 30-APR-2003; 2003US-00427160.
XX 23-MAY-2003; 2003US-00444853.
XX 23-OCT-2003; 2003US-00693059.
XX 24-NOV-2003; 2003US-00720448.
XX 14-JAN-2004; 2004US-00757803.
XX
XX (RICH/) RICHARDS I.
XX (MCSW/) MCSWIGGEN J.
XX
XX Richards I, Mcswiggen J;
XX
XX WPI; 2005-090672/10.
XX
XX Novel chemically synthesized double stranded short interfering nucleic
PT acid molecule that directs cleavage of cholinergic receptor muscarinic 3
PT RNA through RNA interference, useful for treating asthma.
XX
XX Disclosure; SEQ ID NO 315; 84pp; English.
XX
XX The invention relates to a chemically synthesized double stranded short
CC interfering nucleic acid (siNA) molecule (I) that directs cleavage of a
CC cholinergic receptor muscarinic 3 (CHRM3) RNA through RNA interference,
CC where each strand of (I) has 19-23 nucleotides, and does not require the
CC presence of nucleotides having a 2-hydroxy group for mediating RNA
CC interference. (I) is useful for treating diseases e.g., asthma, allergic
CC rhinitis, sinusitis, inflammation, allergy, cystic fibrosis, pulmonary
CC vasoconstriction or hypertension, emphysema, irritable bowel syndrome,
CC Alzheimer's disease or urinary incontinence. (I) has increased resistance
CC towards nuclease. Double stranded short interfering nucleic acid molecule
CC was produced by solid phase oligonucleotide synthesis method. This
CC sequence represents an example of a siRNA molecule of the invention.
XX
XX Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;
XX
XX Query Match 100.0%; Score 14; DB 14; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+03;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 AUAUAUCUAUUUCG 14
Db 1 AUAUAUCUAUUUCG 14
XX
XX RESULT 7
XX ADW73595
XX ID ADW73595 standard; RNA; 14 BP.
XX AC ADW73595;
XX
XX 07-APR-2005 (first entry)
XX
XX Human B7-H1 siRNA target sequence oligonucleotide SeqID295.
XX
XX short interfering RNA; RNA interference; gene silencing; siRNA; B7-H1;
XX cytostatic; vasotropic; nephrotropic; immunomodulator; tumor;
XX immune disorder; proliferative disorder; cancer; restenosis;
XX renal disease; ss.
XX
XX Homo sapiens.
XX

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PN WO2005007855-A2.  
 XX 27-JAN-2005.  
 PD 14-JUL-2004; 2004WO-US022658.  
 XX 14-JUL-2003; 2003US-0487214P.  
 PR 23-OCT-2003; 2003US-00693059.  
 PR 24-NOV-2003; 2003US-00720448.  
 PR 03-DEC-2003; 2003US-00727780.  
 PR 10-JAN-2004; 2004US-00757803.  
 PR 14-FEB-2004; 2004US-0543480P.  
 PR 13-FEB-2004; 2004US-00780447.  
 PR 16-APR-2004; 2004US-00826966.  
 PR 30-APR-2004; 2004WO-US013456.  
 PR 24-MAY-2004; 2004WO-US016390.  
 XX (SIRN-) SIRNA THERAPEUTICS INC.  
 XX Usman N, Mcswiggen J;  
 PI WPI; 2005-112870/12.  
 DR New double stranded short interfering nucleic acid molecule that directs  
 XX cleavage of a B7-H1 RNA, useful for treating tumor-mediated  
 XX immunosuppression, immunopathology and/or proliferative diseases, cancer,  
 XX or restenosis.  
 PS Disclosure; SEQ ID NO 295; 191pp; English.  
 XX This invention relates to a novel chemically synthesized double stranded  
 XX short interfering nucleic acid (siRNA) molecule that directs cleavage of  
 CC a B7-H1 RNA via RNA interference (RNAi), where each strand of the siRNA  
 CC molecule is 18-23 nucleotides in length, and one strand of the siRNA  
 CC molecule comprises nucleotide sequence is complementary to the B7-H1 RNA  
 CC for the siRNA molecule to direct cleavage of the B7-H1 RNA via RNA  
 CC interference. The invention may be useful for the production of compounds  
 CC with a cytostatic, vasotropic, nephrotropic or immunomodulator through  
 CC RNA interference. The siRNA, compounds, compositions, and methods are  
 CC useful for modulating B7-H1 gene expression and for treating tumor-  
 CC mediated immunosuppression, immunopathology and/or proliferative diseases  
 CC and conditions like cancer, restenosis or polycystic kidney disease. The  
 CC present sequence is that of a region of the human B7-H1 which was  
 CC targeted by an siRNA oligonucleotide of the invention.  
 XX Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;  
 SQ Query Match 100.0%; Score 14; DB 14; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 AUAUAUCUAUUUCG 14  
 DB 1 AUAUAUCUAUUUCG 14  
 RESULT 8  
 ADV94764  
 ID ADV94764 standard; RNA; 14 BP.  
 XX ADV94764;  
 AC 07-APR-2005 (first entry)  
 XX Human short interfering nucleic acid SEQ ID NO 1901.  
 XX nontropic; neuroprotective; cerebroprotective; vasotropic;  
 KW cardiovascular-gen.; gene expression; dementia; degeneration;  
 KW Alzheimer's disease; neurodegenerative disease; neurological disease;  
 KW cerebrovascular ischemia; short interfering RNA; siRNA; RNA interference;  
 KW gene silencing; ss.  
 XX Homo sapiens.  
 OS

OS Synthetic.  
 XX WO2005003350-A2.  
 XX 13-JAN-2005.  
 XX 25-JUN-2004; 2004WO-US020516.  
 XX 27-JUN-2003; 2003US-00607933.  
 PR 23-OCT-2003; 2003US-00693059.  
 PR 24-NOV-2003; 2003US-00720448.  
 PR 03-DEC-2003; 2003US-00727780.  
 PR 14-JAN-2004; 2004US-00757803.  
 PR 10-FEB-2004; 2004US-0543480P.  
 PR 13-FEB-2004; 2004US-00780447.  
 PR 16-APR-2004; 2004US-00826966.  
 PR 30-APR-2004; 2004WO-US013456.  
 PR 24-MAY-2004; 2004WO-US016390.  
 XX (SIRN-) SIRNA THERAPEUTICS INC.  
 XX Mcswiggen J, Beigelman L;  
 PI WPI; 2005-091819/10.  
 DR New chemically synthesized double stranded short interfering nucleic acid  
 XX (siRNA) molecule that directs cleavage of an amyloid precursor protein  
 XX (APP) RNA via RNA interference (RNAi), useful for treating Alzheimer's  
 XX disease.  
 PS Disclosure; SEQ ID NO 1901; 233pp; English.  
 XX The invention describes a chemically synthesized double stranded short  
 XX interfering nucleic acid (siRNA) molecule that directs cleavage of an  
 CC amyloid precursor protein (APP) RNA via RNA interference (RNAi). Each  
 CC strand of the siRNA molecule 18-20 nucleotides in length, and one strand  
 CC of the siRNA molecule comprises nucleotide sequence having sufficient  
 CC complementarity to the APP RNA for the siRNA molecule to direct cleavage  
 CC of the APP RNA via RNA interference. Also described is a composition  
 CC comprising the siRNA molecule in a pharmaceutically acceptable carrier or  
 CC diluent. Also disclosed are siRNAs for modulating the expression of other  
 CC genes implicated in Alzheimer's disease and/or dementia, especially beta-  
 CC secretase (BACE), Pin-1, presenilin 1 or presenilin 2. The molecules  
 CC and composition are useful for treating Alzheimer's disease, especially beta-  
 CC neurodegenerative disorders or conditions, and stroke/cardiovascular  
 CC accident in a subject. This sequence represents a short interfering  
 CC nucleic acid (siRNA) used to demonstrate the creation of siRNA's used in  
 CC the invention.  
 XX Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;  
 SQ Query Match 100.0%; Score 14; DB 14; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 AUAUAUCUAUUUCG 14  
 DB 1 AUAUAUCUAUUUCG 14  
 RESULT 9  
 ADV79835  
 ID ADV79835 standard; RNA; 14 BP.  
 XX ADV79835;  
 AC 07-APR-2005 (first entry)  
 XX Exemplary duplex forming RNA oligo, SEQ ID 952.  
 XX short interfering RNA; siRNA; gene silencing; RNA interference;  
 KW anorectic; cardiant; cardiovascular-gen.; antidiabetic; gene therapy;  
 KW obesity; coronary disease; cardiovascular disease; insulin resistance;  
 KW

KW mitochondria; ss.  
XX Synthetic.  
XX WO2005007859-A2.  
PN 27-JAN-2005.  
XX  
XX  
XX 09-JUL-2004; 2004WO-US022247.  
XX  
XX 11-JUL-2003; 2003US-0486729P.  
PR 23-OCT-2003; 2003US-00693059.  
PR 24-NOV-2003; 2003US-00720448.  
PR 03-DEC-2003; 2003US-00727780.  
PR 14-JAN-2004; 2004US-00757803.  
PR 10-FEB-2004; 2004US-0543480P.  
PR 13-FEB-2004; 2004US-0543480P.  
PR 16-APR-2004; 2004US-00826966.  
PR 30-APR-2004; 2004WO-US013456.  
XX  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
PA  
XX Mcswiggen J, Usman N;  
XX WPI; 2005-112874/12.  
XX  
XX New chemically synthesized double stranded short interfering nucleic acid  
PT molecule directing cleavage of acetyl-CoA carboxylase RNA through RNA  
PT interference, useful for treating obesity, cardiovascular disease,  
PT insulin resistance.  
XX  
XX Disclosure; SEQ ID NO 952; 200pp; English.  
XX  
XX The invention relates to a novel, chemically synthesized double stranded  
CC short interfering nucleic acid (siNA) molecule directing cleavage of  
CC acetyl-CoA carboxylase RNA through RNA interference. Each strand of the  
CC siNA molecule is 18-23 nucleotides in length, and one strand has  
CC sufficient nucleotide sequence complementarity to acetyl-CoA carboxylase  
CC RNA for the siNA to direct cleavage of the acetyl-CoA carboxylase RNA  
CC through RNA interference. The invention further comprises: a composition  
CC comprising the siNA and a carrier and diluent; increasing the stability  
CC of an siNA molecule; modulating the expression of acetyl CoA carboxylase  
CC gene within a cell; an expression vector encoding siNA; a mammalian cell  
CC comprising the vector; a kit comprising the siNA; synthesizing an siNA;  
CC active in mediating RNA interference against a target nucleic acid  
CC sequence (sequence of acetyl CoA carboxylase gene). The siNA molecules  
CC have anorectic, cardiant, cardiovascular-gen., and antidiabetic  
CC activities. The siNA molecules may be used in gene therapy. The siNA  
CC molecules are useful for modulating the expression of acetyl-CoA  
CC carboxylase genes associated with the development of obesity,  
CC coronary/cardiovascular disease, insulin resistance and/or mitochondrial  
CC disease. The siNA molecules are useful in therapeutic, diagnostic, target  
CC validation, genomic discovery, genetic engineering, and pharmacogenomic  
CC applications. The siNA molecules and compositions are useful for treating  
CC obesity, coronary/cardiovascular disease, insulin resistance and/or  
CC mitochondrial disease. This polynucleotide sequence represents a duplex  
CC forming RNA oligo used in the exemplification of the invention.  
XX  
XX Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;  
SQ  
Query Match 100.0%; Score 14; DB 14; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 AUAUAUCUAUUUCG 14  
|||||||  
DB 1 AUAUAUCUAUUUCG 14  
RESULT 10  
ADW79836/c  
ID ADW79836 standard; RNA; 14 BP.

XX AC ADW79836;  
XX  
XX 07-APR-2005 (first entry)  
XX  
XX Exemplary duplex forming RNA oligo, SEQ ID 953.  
XX  
XX short interfering RNA; siRNA; gene silencing; RNA interference;  
KW anorectic; cardiant; cardiovascular-gen.; antidiabetic; gene therapy;  
KW obesity; coronary disease; cardiovascular disease; insulin resistance;  
KW mitochondria; ss.  
XX  
XX Synthetic.  
XX WO2005007859-A2.  
XX  
XX 27-JAN-2005.  
XX  
XX 09-JUL-2004; 2004WO-US022247.  
XX  
XX 11-JUL-2003; 2003US-0486729P.  
PR 23-OCT-2003; 2003US-00693059.  
PR 24-NOV-2003; 2003US-00720448.  
PR 03-DEC-2003; 2003US-00727780.  
PR 14-JAN-2004; 2004US-00757803.  
PR 10-FEB-2004; 2004US-0543480P.  
PR 13-FEB-2004; 2004US-00780447.  
PR 16-APR-2004; 2004US-00826966.  
PR 30-APR-2004; 2004WO-US013456.  
XX  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
PA  
XX Mcswiggen J, Usman N;  
XX WPI; 2005-112874/12.  
XX  
XX New chemically synthesized double stranded short interfering nucleic acid  
PT molecule directing cleavage of acetyl-CoA carboxylase RNA through RNA  
PT interference, useful for treating obesity, cardiovascular disease,  
PT insulin resistance.  
XX  
XX Disclosure; SEQ ID NO 953; 200pp; English.  
XX  
XX The invention relates to a novel, chemically synthesized double stranded  
CC short interfering nucleic acid (siNA) molecule directing cleavage of  
CC acetyl-CoA carboxylase RNA through RNA interference. Each strand of the  
CC siNA molecule is 18-23 nucleotides in length, and one strand has  
CC sufficient nucleotide sequence complementarity to acetyl-CoA carboxylase  
CC RNA for the siNA to direct cleavage of the acetyl-CoA carboxylase RNA  
CC through RNA interference. The invention further comprises: a composition  
CC comprising the siNA and a carrier and diluent; increasing the stability  
CC of an siNA molecule; modulating the expression of acetyl CoA carboxylase  
CC gene within a cell; an expression vector encoding siNA; a mammalian cell  
CC comprising the vector; a kit comprising the siNA; synthesizing an siNA;  
CC active in mediating RNA interference against a target nucleic acid  
CC sequence (sequence of acetyl CoA carboxylase gene). The siNA molecules  
CC have anorectic, cardiant, cardiovascular-gen., and antidiabetic  
CC activities. The siNA molecules may be used in gene therapy. The siNA  
CC molecules are useful for modulating the expression of acetyl-CoA  
CC carboxylase genes associated with the development of obesity,  
CC coronary/cardiovascular disease, insulin resistance and/or mitochondrial  
CC disease. The siNA molecules are useful in therapeutic, diagnostic, target  
CC validation, genomic discovery, genetic engineering, and pharmacogenomic  
CC applications. The siNA molecules and compositions are useful for treating  
CC obesity, coronary/cardiovascular disease, insulin resistance and/or  
CC mitochondrial disease. This polynucleotide sequence represents a duplex  
CC forming RNA oligo used in the exemplification of the invention.  
XX  
XX Sequence 14 BP; 7 A; 1 C; 2 G; 0 T; 4 U; 0 Other;  
SQ  
Query Match 100.0%; Score 14; DB 14; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 AUAUAUCUAUUUCG 14  
|||||||  
DB 1 AUAUAUCUAUUUCG 14  
RESULT 10  
ADW79836/c  
ID ADW79836 standard; RNA; 14 BP.

Matches 7; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUAUAUCUAUUCG 14  
 Db 14 ATATATCTATTTCG 1

RESULT 11  
 ID ADV31142/c  
 XX ADV31142; RNA; 14 BP.  
 AC ADV31142;  
 XX 05-MAY-2005 (first entry)  
 DT  
 XX Oligonucleotide, SEQ ID 74, used to illustrate method to produce DFO.  
 DE  
 XX Gene Therapy; DNA detection; RNA detection; ss.  
 KW  
 XX Unidentified.  
 OS  
 XX US2005042632-A1.  
 XX 24-FEB-2005.  
 XX 08-APR-2004; 2004US-00820622.  
 XX 13-FEB-2002; 2002US-0356298P.  
 PR 12-FEB-2003; 2003US-00366191.  
 XX (SIRN-) SIRNA THERAPEUTICS INC.  
 PA  
 XX Radka SF;  
 PI  
 XX WPI; 2005-180795/19.  
 DR  
 XX New isolated antibody having binding affinity for a nucleic acid molecule  
 PT having a 2'-deoxy-2'-fluoro Uridine nucleoside and/or nucleotide, useful  
 PT for treating cancer, viral, inflammatory, or autoimmune diseases.  
 XX  
 PS Disclosure; SEQ ID NO 74; 59pp; English.  
 XX  
 CC The present invention relates to an isolated antibody which has binding  
 CC affinity for a nucleic acid molecule having a 2'-deoxy-2'-fluoro Uridine  
 CC nucleoside and/or nucleotide. The nucleic acid molecule comprises a short  
 CC interfering nucleic acid (siNA), preferably a duplex siNA or a hairpin  
 CC siNA. The antibody is useful for detecting the presence of nucleic acid  
 CC molecules, including siRNA molecules and ribozymes, in vivo. It is also  
 CC useful as screening agents, which allow the selection of candidate  
 CC therapeutic molecules for optimum bioavailability and/or activity, and as  
 CC delivery agents for cell- and tissue-specific delivery of nucleic acid  
 CC molecules. The antibody can also be used for treating cancer (including  
 CC breast, lung, prostate, colorectal, brain, bladder, pancreatic, cervical,  
 CC or ovarian cancer) or viral infections (including HIV, poliovirus,  
 CC influenza, rhinovirus, Ebola virus, or foot and mouth virus). It can also  
 CC be used for treating inflammatory diseases (including chronic  
 CC inflammation, atherosclerosis, restenosis, asthma, atopic dermatitis,  
 CC inflammatory bowel disease, pain, or septic shock) and autoimmune  
 CC diseases (including multiple sclerosis, diabetes, lupus, ulcerative  
 CC colitis, or celiac disease). The compounds and methods above are useful  
 CC for introducing nucleotides, nucleosides, nucleic acid molecules, lipids,  
 CC peptides, proteins, and/or non-nucleosidic small molecules into a cell.  
 CC The present sequence was used to illustrate a method used to design self  
 CC complementary duplex forming oligonucleotide (DFO) constructs using  
 CC palindromic and/or repeat nucleic acid sequences. ADV31141 was the target  
 CC nucleic acid for which the complementary strand was designed (ADV31142).  
 CC The inverse sequence of the non-palindromic complementary sequence of  
 CC ADV31142 was appended to the 3'-end of the complementary sequence to  
 CC produce ADV31143, which could form a duplex construct with blunt ends by  
 CC self assembly of self complementary strands. ADV31144 is another DFO with  
 CC a two nucleotide 3' overhang, or can also form a stem loop construct.  
 XX  
 SQ Sequence 14 BP; 7 A; 1 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 100.0%; Score 14; DB 14; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 2.9e+03;  
 Matches 7; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUAUAUCUAUUCG 14  
 Db 14 ATATATCTATTTCG 1

RESULT 12  
 ID ADV31141  
 XX ADV31141 standard; RNA; 14 BP.  
 AC ADV31141;  
 XX 05-MAY-2005 (first entry)  
 DT  
 XX Oligonucleotide, SEQ ID 73, used to illustrate method to produce DFO.  
 DE  
 XX Gene Therapy; DNA detection; RNA detection; ss.  
 KW  
 XX Unidentified.  
 OS  
 XX US2005042632-A1.  
 XX 24-FEB-2005.  
 XX 08-APR-2004; 2004US-00820622.  
 XX 13-FEB-2002; 2002US-0356298P.  
 PR 12-FEB-2003; 2003US-00366191.  
 XX (SIRN-) SIRNA THERAPEUTICS INC.  
 PA  
 XX Radka SF;  
 PI  
 XX WPI; 2005-180795/19.  
 DR  
 XX New isolated antibody having binding affinity for a nucleic acid molecule  
 PT having a 2'-deoxy-2'-fluoro Uridine nucleoside and/or nucleotide, useful  
 PT for treating cancer, viral, inflammatory, or autoimmune diseases.  
 XX  
 PS Disclosure; SEQ ID NO 73; 59pp; English.  
 XX  
 CC The present invention relates to an isolated antibody which has binding  
 CC affinity for a nucleic acid molecule having a 2'-deoxy-2'-fluoro Uridine  
 CC nucleoside and/or nucleotide. The nucleic acid molecule comprises a short  
 CC interfering nucleic acid (siNA), preferably a duplex siNA or a hairpin  
 CC siNA. The antibody is useful for detecting the presence of nucleic acid  
 CC molecules, including siRNA molecules and ribozymes, in vivo. It is also  
 CC useful as screening agents, which allow the selection of candidate  
 CC therapeutic molecules for optimum bioavailability and/or activity, and as  
 CC delivery agents for cell- and tissue-specific delivery of nucleic acid  
 CC molecules. The antibody can also be used for treating cancer (including  
 CC breast, lung, prostate, colorectal, brain, bladder, pancreatic, cervical,  
 CC or ovarian cancer) or viral infections (including HIV, poliovirus,  
 CC influenza, rhinovirus, Ebola virus, or foot and mouth virus). It can also  
 CC be used for treating inflammatory diseases (including chronic  
 CC inflammation, atherosclerosis, restenosis, asthma, atopic dermatitis,  
 CC inflammatory bowel disease, pain, or septic shock) and autoimmune  
 CC diseases (including multiple sclerosis, diabetes, lupus, ulcerative  
 CC colitis, or celiac disease). The compounds and methods above are useful  
 CC for introducing nucleotides, nucleosides, nucleic acid molecules, lipids,  
 CC peptides, proteins, and/or non-nucleosidic small molecules into a cell.  
 CC The present sequence was used to illustrate a method used to design self  
 CC complementary duplex forming oligonucleotide (DFO) constructs using  
 CC palindromic and/or repeat nucleic acid sequences. ADV31141 was the target  
 CC nucleic acid for which the complementary strand was designed (ADV31142).  
 CC The inverse sequence of the non-palindromic complementary sequence of  
 CC ADV31142 was appended to the 3'-end of the complementary sequence to  
 CC produce ADV31143, which could form a duplex construct with blunt ends by  
 CC self assembly of self complementary strands. ADV31144 is another DFO with  
 CC a self assembly of self complementary strands. ADV31144 is another DFO with

CC a two nucleotide 3' overhang, or can also form a stem loop construct.  
 XX  
 SQ Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;  
 Query Match 100.0%; Score 14; DB 14; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AUAUAUCUAUUUCG 14  
 |||||  
 Db 1 AUAUAUCUAUUUCG 14  
 RESULT 13  
 ADX87169  
 ID ADX87169 standard; RNA; 14 BP.  
 XX  
 AC ADX87169;  
 XX  
 DT 05-MAY-2005 (first entry)  
 XX  
 DE XIAP targeting siRNA SEQ ID NO 1057.  
 XX  
 KW ds; primer; short interfering RNA; siRNA;  
 KW X-linked inhibitor of apoptosis protein; XIAP; RNA interference; RNAi;  
 KW cytostatic; cancer; gene silencing.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2005014811-A2.  
 PN  
 XX  
 PD 17-FEB-2005.  
 XX  
 XX 06-AUG-2004; 2004WO-US025589.  
 XX  
 PR 08-AUG-2003; 2003US-0493561P.  
 PR 23-OCT-2003; 2003US-00693059.  
 PR 24-NOV-2003; 2003US-00720448.  
 PR 03-DEC-2003; 2003US-00727780.  
 PR 14-JAN-2004; 2004US-00757803.  
 PR 10-FEB-2004; 2004US-0543480P.  
 PR 13-FEB-2004; 2004US-00780447.  
 PR 16-APR-2004; 2004US-00826966.  
 PR 30-APR-2004; 2004WO-US013456.  
 PR 24-MAY-2004; 2004WO-US016390.  
 XX  
 PA (SIRN-) SIRNA THERAPEUTICS INC.  
 XX  
 XX Mcswiggen J, Chowrira BM;  
 PI  
 XX WPI; 2005-163247/17.  
 DR  
 XX  
 XX New chemically synthesized double stranded short interfering nucleic acid  
 PT that directs cleavage of an X-linked inhibitor of apoptosis protein  
 PT (XIAP) RNA via RNA interference, useful in preparing a composition for  
 PT treating cancer.  
 XX  
 XX Claim 33; SEQ ID NO 1057; 202pp; English.  
 PS  
 XX This invention describes novel chemically synthesized double stranded  
 CC short interfering nucleic acid (siRNA) molecules which direct cleavage of  
 CC a X-linked inhibitor of apoptosis protein (XIAP) RNA via RNA interference  
 CC (RNAi), where each strand of the siRNA molecule is about 18-23  
 CC nucleotides in length and one strand of the siRNA molecule comprises  
 CC nucleotide sequence having sufficient complementarity to the XIAP RNA.  
 CC The siRNA molecules can be used to make a cytostatic composition  
 CC comprising the siRNA molecule in a carrier or diluent. The sense and  
 CC antisense strands are connected via a linker molecule. The pyrimidine  
 CC nucleotides in the sense region are 2'-O-methyl pyrimidine nucleotides.  
 CC The purine nucleotides in the sense region are 2'-deoxy purine  
 CC nucleotides and the pyrimidine nucleotides are 2'-deoxy-2'-fluoro  
 CC pyrimidine nucleotides. The fragment comprising the sense region includes  
 CC a terminal cap moiety at a 5'-end, a 3'-end, or both of the 5' and 3'

CC ends of the fragment comprising the sense region. The terminal cap moiety  
 CC is an inverted deoxy abasic moiety. The pyrimidine nucleotides of the  
 CC antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the  
 CC purine nucleotides are 2'-O-methyl purine nucleotides. The purine  
 CC nucleotides present in the antisense region comprise 2'-deoxy- purine  
 CC nucleotides. The antisense region comprises a phosphorothioate  
 CC internucleotide linkage at the 3' end of the antisense region. The  
 CC antisense region comprises a glyceryl modification at a 3' end of the  
 CC antisense region. About 19 nucleotides of each fragment of the siRNA  
 CC molecule are base-paired to the complementary nucleotides of the other  
 CC fragment of the siRNA. The 5'-end of the fragment comprising the  
 CC antisense region optionally includes a phosphate group. The XIAP RNA  
 CC comprises Genbank Accession No. NM\_001167. The chemically synthesized  
 CC double stranded short interfering nucleic acid (siRNA) molecule is useful  
 CC in preparing a composition for treating cancer. ADX86130-ADX87180  
 CC represent siRNA molecules which are used in RNA interference mediated  
 CC inhibition of XIAP gene expression.  
 XX  
 XX Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 14; DB 14; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AUAUAUCUAUUUCG 14  
 |||||  
 Db 1 AUAUAUCUAUUUCG 14  
 RESULT 14  
 ADY91198  
 ID ADY91198 standard; RNA; 14 BP.  
 XX  
 AC ADY91198;  
 XX  
 DT 16-JUN-2005 (first entry)  
 XX  
 DE VEGF/VEGFR DFO siRNA SEQ ID NO 4249.  
 XX  
 KW ss; siRNA; short interfering RNA; RNA interference; gene silencing; VEGF;  
 KW pharmaceutical; cancer; neoplasm; Cytostatic; VEGFR.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2005028649-A1.  
 PN  
 XX  
 PD 31-MAR-2005.  
 XX  
 XX 16-SEP-2004; 2004WO-US030488.  
 XX  
 PR 16-SEP-2003; 2003US-00664767.  
 PR 16-SEP-2003; 2003US-00665255.  
 PR 23-SEP-2003; 2003US-00670011.  
 PR 23-OCT-2003; 2003US-00693059.  
 PR 24-NOV-2003; 2003US-00720448.  
 PR 03-DEC-2003; 2003US-00727780.  
 PR 14-JAN-2004; 2004US-00757803.  
 PR 26-JAN-2004; 2004US-00764957.  
 PR 10-FEB-2004; 2004US-0543480P.  
 PR 13-FEB-2004; 2004US-00780447.  
 PR 16-APR-2004; 2004US-00826966.  
 PR 23-APR-2004; 2004US-00831620.  
 PR 30-APR-2004; 2004US-00013456.  
 PR 11-MAY-2004; 2004US-00844076.  
 XX  
 XX (SIRN-) SIRNA THERAPEUTICS INC.  
 PA  
 XX Jadhav V, Kossen K, Zinnen S, Vaish N, Mcswiggen J;  
 PI WPI; 2005-254128/26.  
 XX  
 XX New multifunctional siNA molecule that directs cleavage of the first and  
 PT second VEGF or VEGFR target sequences via RNA interference, useful in

PT preparing a composition for treating cell proliferative disorders e.g.  
PT cancers.  
XX  
PS Disclosure; SEQ ID NO 4249; 396pp; English.  
XX  
CC The invention relates to a multifunctional siNA molecule comprising a  
CC structure having Formula MF-III and which directs cleavage of the first  
CC and second VEGF or VEGFR target sequences via RNA interference. The  
CC multifunctional siNA molecule is useful in preparing a pharmaceutical  
CC composition for treating cell proliferative disorders, e.g. cancer. The  
CC present sequence represents a VEGF/VEGFR DFO siRNA.  
XX  
SQ Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;  
Query Match 100.0%; Score 14; DB 14; Length 14;  
Best Local Similarity 100.0%; Pred. NO. 2.9e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AUAUAUCUAUUUCG 14  
Db 1 AUAUAUCUAUUUCG 14  
RESULT 15  
ADZ02756  
ID ADZ02756 standard; RNA; 14 BP.  
XX  
AC ADZ02756;  
XX  
DT 16-JUN-2005 (first entry)  
XX  
DE Hepatitis C virus short interfering nucleic acid SEQ ID NO 2028.  
XX  
KW antiinflammatory; hepatotropic; virucide; gene therapy; RNA Interference;  
KW gene silencing; antisense therapy; antisense oligonucleotide;  
KW pharmaceutical; gene expression; hepatitis C virus infection;  
KW gastrointestinal disease; infection; siRNA; short interfering RNA; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2005028650-A2.  
XX  
PD 31-MAR-2005.  
XX  
PF 15-SEP-2004; 2004WO-US031012.  
XX  
PR 16-SEP-2003; 2003US-00667271.  
PR 23-OCT-2003; 2003US-00693059.  
PR 24-NOV-2003; 2003US-00720448.  
PR 03-DEC-2003; 2003US-00727780.  
PR 14-JAN-2004; 2004US-00757803.  
PR 10-FEB-2004; 2004US-0543480P.  
PR 13-FEB-2004; 2004US-00780447.  
PR 16-APR-2004; 2004US-00826966.  
PR 30-APR-2004; 2004WO-US013456.  
PR 24-MAY-2004; 2004WO-US016390.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Jadhav V, Kossen K, Zinnen S, Vaish N, Mcswiggen J;  
XX  
XX WPI; 2005-254129/26.  
XX  
PT New multifunctional siNA molecule that directs cleavage of the first and  
PT second hepatitis C virus (HCV) target sequences via RNA interference,  
PT useful in preparing a composition for treating hepatitis C virus (HCV)  
PT infection.  
XX  
PS Disclosure; SEQ ID NO 2028; 300pp; English.  
XX  
CC The invention describes a new multifunctional siNA molecule comprises a  
CC structure having Formula MF-III and directs cleavage of the first and  
CC second hepatitis C virus (HCV) target sequences via RNA interference.

CC Also described is a pharmaceutical composition comprising the  
CC multifunctional siNA molecule and a carrier or diluent. The  
CC multifunctional siNA molecule is useful in preparing a pharmaceutical  
CC composition for treating hepatitis C virus (HCV) infection. This sequence  
CC represents a short interfering nucleic acid (siNA) used to control HCV  
CC gene expression.  
XX  
SQ Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;  
Query Match 100.0%; Score 14; DB 14; Length 14;  
Best Local Similarity 100.0%; Pred. NO. 2.9e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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us-10-824-036a-3578.sz40.rn1

Thu Jun 29 15:49:22 2006

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Total number of hits satisfying chosen parameters: 1304306

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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- 4: /EMC Celerra\_SIDS3/ptodata/2/ina/6B COMB.seq:\*
- 5: /EMC Celerra\_SIDS3/ptodata/2/ina/7 COMB.seq:\*
- 6: /EMC Celerra\_SIDS3/ptodata/2/ina/H COMB.seq:\*
- 7: /EMC Celerra\_SIDS3/ptodata/2/ina/PCTUS COMB.seq:\*
- 8: /EMC Celerra\_SIDS3/ptodata/2/ina/PP COMB.seq:\*
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- 10: /EMC Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	12.4	88.6	24	3	US-09-392-486-1
C 2	12	85.7	36	3	US-09-735-271-1975
C 3	12	85.7	38	5	US-10-156-306B-1236
C 4	12	85.7	39	2	US-08-369-829A-11
C 5	12	85.7	39	2	US-08-586-676E-15
C 6	11.4	81.4	20	3	US-10-177-573-44
C 7	11.4	81.4	25	3	US-09-396-196G-40617
C 8	11.4	81.4	26	3	US-09-814-134A-7
C 9	11.4	81.4	33	3	US-08-817-926-38
C 10	11.4	81.4	33	3	US-09-297-053-5
C 11	11	78.6	24	3	US-08-262-220-2
C 12	11	78.6	24	3	US-08-471-733-2
C 13	11	78.6	24	3	US-08-468-878-2
C 14	11	78.6	24	3	US-08-750-494-2
C 15	11	78.6	24	3	US-08-470-638-2
C 16	11	78.6	25	2	US-08-257-781-15
C 17	11	78.6	25	3	US-09-396-196G-24676
C 18	11	78.6	25	7	PCT-US95-06857-15
C 19	11	78.6	34	3	US-09-565-808-6
C 20	11	78.6	36	2	US-08-585-684B-596
C 21	11	78.6	36	3	US-09-038-073-596
C 22	11	78.6	38	5	US-10-156-306B-5493
C 23	10.8	77.1	16	2	US-08-192-941-8

24	10.8	77.1	19	3	US-08-850-961-25	Sequence 25, Appl
25	10.8	77.1	19	3	US-09-479-776-25	Sequence 25, Appl
26	10.8	77.1	20	3	US-09-418-980-24	Sequence 24, Appl
27	10.8	77.1	21	2	US-08-184-941-8	Sequence 8, Appl
28	10.8	77.1	22	3	US-08-850-961-4	Sequence 4, Appl
29	10.8	77.1	22	3	US-09-479-776-4	Sequence 4, Appl
C 30	10.8	77.1	25	3	US-09-396-196G-69848	Sequence 69848, A
C 31	10.8	77.1	30	3	US-09-027-169-11	Sequence 11, Appl
C 32	10.8	77.1	33	3	US-09-417-197-33	Sequence 33, Appl
C 33	10.8	77.1	36	2	US-08-089-458B-1	Sequence 9, Appl
C 34	10.8	77.1	38	2	US-07-805-564A-9	Sequence 9, Appl
C 35	10.8	77.1	38	2	US-08-114-301-9	Sequence 7, Appl
C 36	10.8	77.1	38	2	PCT-US92-10431-9	Sequence 55, Appl
C 37	10.8	77.1	40	2	US-08-425-684-7	Sequence 7, Appl
C 38	10.8	77.1	40	2	US-08-675-502-7	Sequence 55, Appl
C 39	10.8	77.1	40	2	US-08-675-502-55	Sequence 7, Appl
C 40	10.8	77.1	40	3	US-09-245-802-7	Sequence 55, Appl
C 41	10.8	77.1	40	3	US-09-245-802-55	Sequence 42, Appl
C 42	10.8	77.1	21	7	PCT-US91-03680-42	Sequence 489, App
C 43	10.6	75.7	16	3	US-09-479-005A-489	Sequence 490, App
C 44	10.4	74.3	16	3	US-09-479-005A-489	
C 45	10.4	74.3	16	3	US-09-479-005A-490	

ALIGNMENTS

RESULT 1  
US-09-392-486-1/c  
; Sequence 1, Application US/09392486  
; Patent No. 6255054  
; GENERAL INFORMATION:  
; APPLICANT: HUGON, Jacques  
; APPLICANT: BACLET, Marie-Claire  
; TITLE OF INVENTION: POLYMORPHISM OF THE HUMAN GluR-5 GENE AND RISK FACTOR  
; FILE REFERENCE: R-340205  
; CURRENT APPLICATION NUMBER: US/09/392,486  
; CURRENT FILING DATE: 1999-09-09  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.2  
; SEQ ID NO 1  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer derived from Human glutamate (Kainate) receptor 5 (GluR-5)  
US-09-392-486-1

Query Match 88.6%; Score 12.4; DB 3; Length 24;  
Best Local Similarity 42.9%; Pred. No. 4.6e+03;  
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Oy 1 AUAUUAUUUUG 14  
|:|:|:|:|:  
Db 15 ATATATCTATTAG 2

RESULT 2  
US-09-735-271-1975  
; Sequence 1975, Application US/09735271  
; Patent No. 6869762  
; GENERAL INFORMATION:  
; APPLICANT: Daly, Mark J.  
; APPLICANT: Hudson, Thomas J.  
; APPLICANT: Rioux, John  
; APPLICANT: Lander, Eric S.  
; APPLICANT: Siminovich, Kathy  
; TITLE OF INVENTION: IBD-RELATED POLYMORPHISMS  
; FILE REFERENCE: 2825.1025-002  
; CURRENT APPLICATION NUMBER: US/09/735,271  
; CURRENT FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 60/170,257

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; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/196,046
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 2058
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1975
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(36)
; OTHER INFORMATION: n = A,T,C or G
US-09-735-271-1975

Query Match      85.7%; Score 12; DB 3; Length 36;
Best Local Similarity 38.5%; Pred. No. 7e+03;
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY      1 AUAUAUCUAUUC 13
Db      10 ATATATNTATTC 22

RESULT 3
US-10-156-306B-1236/c
; Sequence 1236, Application US/10156306B
; Patent No. 7022828
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306B
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1236
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-156-306B-1236

Query Match      85.7%; Score 12; DB 5; Length 38;
Best Local Similarity 50.0%; Pred. No. 7e+03;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      3 AUAUAUCUAUUC 14
Db      38 ATATCTATTTCG 27

RESULT 4
US-08-369-829A-11
; Sequence 11, Application US/08369829A
; Patent No. 5861377
; GENERAL INFORMATION:
; APPLICANT: Hans Fritz
; APPLICANT: Christian Sommerhoff
; APPLICANT: Jutta Heim
; TITLE OF INVENTION: No. 5861377el Inhibitor
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5861377artis Corporation
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: US
; ZIP: 07936
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,829A
; FILING DATE: 6-JAN-95
; PRIOR APPLICATION DATA: EPO 94810006.0
; APPLICATION NUMBER: 7-JAN-94
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5861377ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-19942/A/DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..39
; OTHER INFORMATION: /function= "synthetic oligo for PCR"
US-08-369-829A-11

Query Match      85.7%; Score 12; DB 2; Length 39;
Best Local Similarity 50.0%; Pred. No. 7e+03;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      3 AUAUAUCUAUUC 14
Db      28 ATATCTATTTCG 39

RESULT 5
US-08-586-676B-15
; Sequence 15, Application US/08586676E
; Patent No. 5972698
; GENERAL INFORMATION:
; APPLICANT: Fritz, Hans,
; APPLICANT: Sommerhoff, Christian
; TITLE OF INVENTION: Trypsin Inhibitor
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5972698artis Corporation, Patent and Trademark Department
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: US
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,676E
; FILING DATE: 25-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/02445
; FILING DATE: 25-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93111930.9
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pfeiffer, Henna J.
; REGISTRATION NUMBER: 22,640
; REFERENCE/DOCKET NUMBER: 4-20076/PCT
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TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 522 6940  
TELEFAX: (908) 522 6955  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: synthetic DNA  
US-08-586-676E-15

Query Match 85.7%; Score 12; DB 2; Length 39;  
Best Local Similarity 50.0%; Pred. No. 7e+03; 0; Indels 0; Gaps 0;  
Matches 6; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 3 AUAUCUAUUCG 14  
|:|:|:|:|:|  
Db 28 ATATCTATTTCG 39

RESULT 6  
US-10-177-573-44  
Sequence 44, Application US/10177573  
Patent No. 6828149  
GENERAL INFORMATION:  
APPLICANT: Susan M. Freier  
TITLE OF INVENTION: ANTISENSE MODULATION OF PPP3R1 EXPRESSION  
FILE REFERENCE: RTS-0364  
CURRENT APPLICATION NUMBER: US/10/177,573  
CURRENT FILING DATE: 2002-06-20  
NUMBER OF SEQ ID NOS: 104  
SEQ ID NO 44  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-10-177-573-44

Query Match 81.4%; Score 11.4; DB 3; Length 20;  
Best Local Similarity 46.2%; Pred. No. 1.4e+04;  
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUACUAUUC 13  
|:|:|:|:|:|  
Db 2 ATATATCTATTAC 14

RESULT 7  
US-09-396-196G-40617  
Sequence 40617, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Wittmann  
APPLICANT: David Meck  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 40617  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-396-196G-40617

Query Match 81.4%; Score 11.4; DB 3; Length 25;

Best Local Similarity 38.5%; Pred. No. 1.4e+04;  
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUACUAUUC 13  
|:|:|:|:|:|  
Db 1 ATTATCTATTTC 13

RESULT 8  
US-09-814-134A-7/c  
Sequence 7, Application US/09814134A  
Patent No. 6395531  
GENERAL INFORMATION:  
APPLICANT: Kong, Huimin  
APPLICANT: Higgins, Lauren Sears  
TITLE OF INVENTION: Method For Cloning And Expression of MlyI Restriction  
TITLE OF INVENTION: Endonuclease And MlyI Methylase And BetNBII Methylase  
TITLE OF INVENTION: in E. coli  
FILE REFERENCE: NEB-186  
CURRENT APPLICATION NUMBER: US/09/814,134A  
CURRENT FILING DATE: 2001-03-21  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 26  
TYPE: DNA  
ORGANISM: Micrococcus lylae  
US-09-814-134A-7

Query Match 81.4%; Score 11.4; DB 3; Length 26;  
Best Local Similarity 46.2%; Pred. No. 1.4e+04;  
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUACUAUUC 13  
|:|:|:|:|:|  
Db 24 ATATATCTAATTC 12

RESULT 9  
US-08-817-926-38/c  
Sequence 38, Application US/08817926  
Patent No. 6001590  
GENERAL INFORMATION:  
APPLICANT: Kameda, Toshihiro  
APPLICANT: Suda, Hisako  
APPLICANT: Tamai, Yukio  
APPLICANT: Iwamatsu, Akihiro  
APPLICANT: Kato, No. 6001590uo  
APPLICANT: Sakai, Yasuyoshi  
TITLE OF INVENTION: PROMOTER/TERMINATOR FOR CANDIDA BOIDINII  
TITLE OF INVENTION: FORMATE DEHYDROGENASE GENE  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,926  
FILING DATE: 09-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP96/02597  
FILING DATE: 12-SEP-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 234133/1995

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; FILING DATE: 12-SEP-1995
; PRIOR APPLICATION DATA: JP 42536/1996
; FILING DATE: 29-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 081356/0112
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 9041136
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
;
US-08-817-926-38

Query Match 81.4%; Score 11.4; DB 3; Length 33;
Best Local Similarity 38.5%; Pred. No. 1.4e+04;
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AUAUAUCUAUUC 13
Db 22 ATGTATCTATTTC 10

RESULT 10
US-09-297-053-5/c
; Sequence 5, Application US/09297053
; Patent No. 6274340
; GENERAL INFORMATION:
; APPLICANT: KOMEDA, Toshihiro
; TITLE OF INVENTION: DNA SEQUENCE INCREASING PROMOTER ACTIVITY
; FILE REFERENCE: 081356/0131
; CURRENT APPLICATION NUMBER: US/09/297,053
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: PCT/JP98/03848
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: JP 9-234995
; EARLIER FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
;
US-09-297-053-5

Query Match 81.4%; Score 11.4; DB 3; Length 33;
Best Local Similarity 38.5%; Pred. No. 1.4e+04;
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AUAUAUCUAUUC 13
Db 22 ATGTATCTATTTC 10

RESULT 11
US-08-262-220-2/c
; Sequence 2, Application US/08262220
; Patent No. 6054296
; GENERAL INFORMATION:
; APPLICANT: BERGSTROM SVEN
; APPLICANT: BARBOUR ALAN G.
; TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA
; NUMBER OF SEQUENCES: 14
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 SEVENTH STREET, N.W.
; CITY: WASHINGTON
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/262,220
; FILING DATE: 20-JUN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: BERGSTROM-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-262-220-2

Query Match 78.6%; Score 11; DB 3; Length 24;
Best Local Similarity 38.5%; Pred. No. 2.2e+04;
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AUAUAUCUAUUC 13
Db 13 AWATATCTTTTC 1

RESULT 12
US-08-471-733-2/c
; Sequence 2, Application US/08471733
; Patent No. 6068842
; GENERAL INFORMATION:
; APPLICANT: BERGSTROM SVEN
; APPLICANT: BARBOUR ALAN G.
; TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 SEVENTH STREET, N.W.
; CITY: WASHINGTON
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,733
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/262,220
; FILING DATE: 20-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: BERGSTROM-3
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-471-733-2

Query Match 78.6%; Score 11; DB 3; Length 24;  
Best Local Similarity 38.5%; Pred. No. 2.2e+04;  
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUACUUAUUC 13  
Db 13 AWATATCTTTTC 1

## RESULT 13

US-08-468-878-2/c  
Sequence 2, Application US/08468878  
Patent No. 6090586  
GENERAL INFORMATION:  
APPLICANT: BERGSTROM SVEN  
APPLICANT: BARBOUR ALAN G.  
TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 SEVENTH STREET, N.W.  
CITY: WASHINGTON  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,878  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/262,220  
FILING DATE: 20-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: COOPER, IVER P.  
REGISTRATION NUMBER: 28,005  
REFERENCE/DOCKET NUMBER: BERGSTROM=3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-468-878-2

Query Match 78.6%; Score 11; DB 3; Length 24;  
Best Local Similarity 38.5%; Pred. No. 2.2e+04;  
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUACUUAUUC 13  
Db 13 AWATATCTTTTC 1

RESULT 14  
US-08-750-494-2/c  
Sequence 2, Application US/08750494  
Patent No. 6204018  
GENERAL INFORMATION:  
APPLICANT: BERGSTROM SVEN  
APPLICANT: BARBOUR ALAN G.  
TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 SEVENTH STREET, N.W.  
CITY: WASHINGTON  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/750,494  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/262,220  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: COOPER, IVER P.  
REGISTRATION NUMBER: 28,005  
REFERENCE/DOCKET NUMBER: BERGSTROM=3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-750-494-2

Query Match 78.6%; Score 11; DB 3; Length 24;  
Best Local Similarity 38.5%; Pred. No. 2.2e+04;  
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUACUUAUUC 13  
Db 13 AWATATCTTTTC 1

## RESULT 15

US-08-470-638-2/c  
Sequence 2, Application US/08470638  
Patent No. 6509017  
GENERAL INFORMATION:  
APPLICANT: BERGSTROM SVEN  
APPLICANT: BARBOUR ALAN G.  
TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 SEVENTH STREET, N.W.  
CITY: WASHINGTON  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,638
; FILING DATE: 06-06-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/262,220
; FILING DATE: 20-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: BERGSTROM=3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-470-638-2

Query Match          78.6%; Score 11; DB 3; Length 24;
Best Local Similarity 38.5%; Pred. No. 2.2e+04;
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY      1 AUUAUUCUAUUC 13
Db      13 AWATATCTTTTC 1
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Search completed: June 28, 2006, 23:31:41  
Job time : 97 secs

November 2005

Published Applications Nucleic Acid and Published Applications Amino Acid database searches now generate two sets of results each. The Published Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published Applications New databases: older published applications make up the Published Applications Main databases.

Searches run against Nucleic Acid Published Applications produce two sets of results, with the extensions **.rapbm** (Published Applications NA Main) and **.rnpbm** (Published Applications NA New).  
Searches run against Amino Acid Published Applications produce two sets of results, with the extensions **.rapbm** (Published Applications AA Main) and **.rnpbm** (Published Applications AA New).

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Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: June 28, 2006, 23:30:19 ; Search time 818 Seconds  
(without alignments)  
210.302 Million cell updates/sec  
Title: US-10-824-036A-3578  
Perfect score: 14  
Sequence: 1 AUAUAUCUAUUCG 14  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 18992170 seqs, 6143817638 residues  
Total number of hits satisfying chosen parameters: 23675114  
Minimum DB seq length: 0  
Maximum DB seq length: 40  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:  
1: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*  
2: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*  
3: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*  
4: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*  
5: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*  
6: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*  
7: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
8: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
9: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*  
10: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*  
11: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*  
12: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*  
13: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*  
14: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*  
15: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US11C\_PUBCOMB.seq.\*  
16: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

ALIGNMENTS  
RESULT 1  
US-10-820-622-73  
; Sequence 73, Application US/10820622  
; Publication No. US20050042632A1  
; GENERAL INFORMATION:  
; APPLICANT: Surna Therapeutics, Inc.  
; TITLE OF INVENTION: Antibodies Having Specificity for Nucleic Acids  
; FILE REFERENCE: 900/051 (MBH02-030-B)  
; CURRENT APPLICATION NUMBER: US/10/820,622  
; CURRENT FILING DATE: 2004-04-08  
; PRIOR APPLICATION NUMBER: US 10/366,191  
; PRIOR FILING DATE: 2003-02-12  
; PRIOR APPLICATION NUMBER: US 60/356,298  
; PRIOR FILING DATE: 2002-02-13  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 73  
; LENGTH: 14  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: siNA target region  
US-10-820-622-73

Query Match 100.0%; Score 14; DB 9; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AUAUAUCUAUUCG 14  
| | | | | | | | | | | | | |  
Db 1 AUAUAUCUAUUCG 14  
RESULT 2  
US-10-820-622-74/c  
; Sequence 74, Application US/10820622  
; Publication No. US20050042632A1  
; GENERAL INFORMATION:  
; APPLICANT: Surna Therapeutics, Inc.

Result No.	Score	Query Match	Length	DB	ID	Description
1	14	100.0	14	9	US-10-820-622-73	Sequence 73, Appl
2	14	100.0	14	9	US-10-820-622-74	Sequence 74, Appl
3	14	100.0	14	10	US-10-894-475-419	Sequence 419, App
4	14	100.0	14	10	US-10-923-115-355	Sequence 355, App
5	14	100.0	14	10	US-10-869-638-467	Sequence 467, App
6	14	100.0	14	10	US-10-871-222-703	Sequence 703, App
7	14	100.0	14	10	US-10-879-867-437	Sequence 437, App
8	14	100.0	14	10	US-10-883-218-927	Sequence 927, App
9	14	100.0	14	10	US-10-888-226-952	Sequence 952, App
10	14	100.0	14	10	US-10-892-922-293	Sequence 293, App
11	14	100.0	14	10	US-10-881-118-449	Sequence 449, App
12	14	100.0	14	10	US-10-861-060-371	Sequence 371, App
13	14	100.0	14	10	US-10-863-973-1829	Sequence 1829, App
14	14	100.0	14	10	US-10-922-544-471	Sequence 471, App
15	14	100.0	14	10	US-10-923-330-765	Sequence 765, App
16	14	100.0	14	10	US-10-916-095-187	Sequence 187, App
17	14	100.0	14	10	US-10-916-095-188	Sequence 188, App

```
; APPLICANT: Susan, Radka
; TITLE OF INVENTION: Antibodies Having Specificity for Nucleic Acids
; FILE REFERENCE: 900/051 (MBHB02-030-B)
; CURRENT APPLICATION NUMBER: US/10/820,622
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 10/366,191
; PRIOR FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: US 60/356,298
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 74
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA complementary region
US-10-820-622-74

Query Match      100.0%; Score 14; DB 9; Length 14;
Best Local Similarity 50.0%; Pred. No. 6.5e+03;
Matches 7; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 AUAUAUCUAUUUCG 14
       |||:|:|:|:|:|
Db      14 ATATATCTATTTCG 1

RESULT 3
US-10-894-475-419
; Sequence 419, Application US/10894475
; Publication No. US20050070497A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Beigelman, James
; APPLICANT: McSwiggen, Leonid
; APPLICANT: Usman, Nassim
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Protein Tyrosine
; TITLE OF INVENTION: Phosphatase-1B (PTP-1B) Gene Expression Using Short Interfering
; FILE REFERENCE: 02-738-F (400/169)
; CURRENT APPLICATION NUMBER: US/10/894,475
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: PCT/US 03/04123
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 10/206,705
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: PCT/US 04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: PCT/US 03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US 03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 419
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: target sequence for
; OTHER INFORMATION: duplex forming oligonucleotide

US-10-894-475-419
Query Match      100.0%; Score 14; DB 9; Length 14;
Best Local Similarity 50.0%; Pred. No. 6.5e+03;
Matches 7; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 AUAUAUCUAUUUCG 14
       |||:|:|:|:|:|
Db      14 ATATATCTATTTCG 1

RESULT 4
US-10-923-115-355
; Sequence 355, Application US/10923115
; Publication No. US20050079610A1
; GENERAL INFORMATION:
; APPLICANT: Polisky, Barry
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of FOS Gene Expression
; FILE REFERENCE: 400/193 (MBHB03-194-A)
; CURRENT APPLICATION NUMBER: US/10/923,115
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US 03/05162
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US 04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 355
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-923-115-355

Query Match      100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AUAUAUCUAUUUCG 14
       |||:|:|:|:|:|
Db      1 AUAUAUCUAUUUCG 14

RESULT 5
US-10-869-638-467
; Sequence 467, Application US/10869638
; Publication No. US20050119211A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Bharat, Chowhira
; APPLICANT: James, McSwiggen
```

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; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Connexin Gene Expression
; TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/165 (MEHB04-503)
; CURRENT APPLICATION NUMBER: US/10/869,638
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 467
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-869-638-467

Query Match 100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 AUAUACUUAUUCG 14
DB 1 AUAUACUUAUUCG 14

RESULT 6
US-10-871-222-703
; Sequence 703, Application US/10871222
; Publication No. US20050119212A1
; GENERAL INFORMATION:
; APPLICANT: Haerberli, Peter
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Mediated Inhibition Fatty Acid Synthase (FAS) and Fatty Acids
; TITLE OF INVENTION: Synthase Ligand (FASL) Gene Expression Using Short Interfering
; TITLE OF INVENTION: Nucleic Acid (siNA)
; FILE REFERENCE: 400/164 (MEHB04-487)
; CURRENT APPLICATION NUMBER: US/10/871,222
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US10/826966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US10/757803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US10/720448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US10/693059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US10/444853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 467
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-869-638-467

Query Match 100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 AUAUACUUAUUCG 14
DB 1 AUAUACUUAUUCG 14

RESULT 7
US-10-879-867-437
; Sequence 437, Application US/10879867
; Publication No. US20050124566A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Robin, Howard
; APPLICANT: Gueriolini, Roberto
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Myostatin Gene Expression
; FILE REFERENCE: 400/196 (MEHB04-536)
; CURRENT APPLICATION NUMBER: US/10/879,867
; CURRENT FILING DATE: 2004-06-28
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 437
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-879-867-437

Query Match 100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 AUAUACUUAUUCG 14
DB 1 AUAUACUUAUUCG 14
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; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US60/358580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US60/363124
; PRIOR FILING DATE: 2002-03-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 706
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 703
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-871-222-703

Query Match 100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 AUAUACUUAUUCG 14
DB 1 AUAUACUUAUUCG 14

RESULT 7
US-10-879-867-437
; Sequence 437, Application US/10879867
; Publication No. US20050124566A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Robin, Howard
; APPLICANT: Gueriolini, Roberto
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Myostatin Gene Expression
; FILE REFERENCE: 400/196 (MEHB04-536)
; CURRENT APPLICATION NUMBER: US/10/879,867
; CURRENT FILING DATE: 2004-06-28
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 437
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-879-867-437

Query Match 100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 AUAUACUUAUUCG 14
DB 1 AUAUACUUAUUCG 14
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUCUAUUUCG 14  
|||||  
Db 1 AUAUAUCUAUUUCG 14

## RESULT 8

US-10-883-218-927  
; Sequence 927, Application US/10883218  
; Publication No. US20050124567A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Haerberli, Peter  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of TRPM7 Gene Expression  
; TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)  
; FILE REFERENCE: 400/195 (MBHB04-535)  
; CURRENT APPLICATION NUMBER: US/10/883,218  
; CURRENT FILING DATE: 2004-07-01  
; PRIOR APPLICATION NUMBER: PCT/US04/16390  
; PRIOR FILING DATE: 2003-05-24  
; PRIOR APPLICATION NUMBER: US 10/826,966  
; PRIOR FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US 10/757,803  
; PRIOR FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US 10/720,448  
; PRIOR FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: US 10/693,059  
; PRIOR FILING DATE: 2003-10-23  
; PRIOR APPLICATION NUMBER: US 10/444,853  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: US 10/427,160  
; PRIOR FILING DATE: 2003-04-30  
; PRIOR APPLICATION NUMBER: PCT/US03/05346  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: PCT/US03/05028  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 930  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 927  
; LENGTH: 14  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence  
US-10-883-218-927

Query Match 100.0%; Score 14; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUCUAUUUCG 14  
|||||  
Db 1 AUAUAUCUAUUUCG 14

## RESULT 9

US-10-888-226-952  
; Sequence 952, Application US/10888226  
; Publication No. US20050124569A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Usman, Nessim  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Acetyl-CoA-Carboxylase  
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)  
; FILE REFERENCE: 400-199 (MBHB03-710-A)  
; CURRENT APPLICATION NUMBER: US/10/888,226  
; CURRENT FILING DATE: 2004-07-09

; PRIOR APPLICATION NUMBER: US 60/486,729  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/US04/16390  
; PRIOR FILING DATE: 2004-05-24  
; PRIOR APPLICATION NUMBER: US 10/826,966  
; PRIOR FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US 10/757,803  
; PRIOR FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US 10/720,448  
; PRIOR FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: US 10/693,059  
; PRIOR FILING DATE: 2003-10-23  
; PRIOR APPLICATION NUMBER: US 10/444,853  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: PCT/US03/05346  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: PCT/US03/05028  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: US 60/358580  
; PRIOR FILING DATE: 2002-02-20  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 955  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 952  
; LENGTH: 14  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence  
US-10-888-226-952

Query Match 100.0%; Score 14; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUCUAUUUCG 14  
|||||  
Db 1 AUAUAUCUAUUUCG 14

## RESULT 10

US-10-892-922-293  
; Sequence 293, Application US/10892922  
; Publication No. US20050124569A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Guercioli, Roberto  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of CXCR4 Gene Expression  
; TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)  
; FILE REFERENCE: 400-198  
; CURRENT APPLICATION NUMBER: US/10/892,922  
; CURRENT FILING DATE: 2004-07-16  
; NUMBER OF SEQ ID NOS: 296  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 293  
; LENGTH: 14  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence  
US-10-892-922-293

Query Match 100.0%; Score 14; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUCUAUUUCG 14  
|||||  
Db 1 AUAUAUCUAUUUCG 14

## RESULT 11

US-10-881-118-449  
; Sequence 449, Application US/10881118  
; Publication No. US20050130181A1  
; GENERAL INFORMATION:  
; APPLICANT: McSwiggen, James  
; APPLICANT: Sirna Therapeutics, Inc.  
; TITLE OF INVENTION: RNA Mediated Inhibition of Wingless Gene Expression Using Short  
; TITLE OF INVENTION: Interfering Nucleic Acid (siNA)  
; FILE REFERENCE: 400-197 (MHBB04-546)  
; CURRENT FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: US/10/881,118  
; PRIOR FILING DATE: 2004-05-24  
; PRIOR APPLICATION NUMBER: PCT/US04/16390  
; PRIOR FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US10/826966  
; PRIOR FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US10/757803  
; PRIOR FILING DATE: 2003-10-23  
; PRIOR APPLICATION NUMBER: US10/693059  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: PCT/US03/05346  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: US10/44853  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: PCT/US03/05028  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: US10/720448  
; PRIOR FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: US60/358580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US60/363124  
; PRIOR FILING DATE: 2002-03-11  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 452  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 449  
; LENGTH: 14  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence  
US-10-881-118-449

Query Match 100.0%; Score 14; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUACUUAUUCG 14  
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Db 1 AUAUACUUAUUCG 14

RESULT 12  
US-10-861-060-371  
; Sequence 371, Application US/10861060  
; Publication No. US20050137155A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: McSwiggen, James  
; APPLICANT: Haerberli, Peter  
; APPLICANT: Chowhira, Bharat  
; TITLE OF INVENTION: RNA Interference Mediated Treatment of Parkinson Disease Using  
; TITLE OF INVENTION: Short Interfering Nucleic Acid (siNA)  
; FILE REFERENCE: 400/162 (MHBB04-372-A)  
; CURRENT FILING DATE: 2004-06-03  
; PRIOR APPLICATION NUMBER: US/10/861,060  
; PRIOR FILING DATE: 2003-10-31  
; PRIOR APPLICATION NUMBER: US 10/698,311  
; PRIOR FILING DATE: 2003-10-31  
; PRIOR APPLICATION NUMBER: US 10/826,966  
; PRIOR FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US 10/757,803  
; PRIOR FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US 10/720,448  
; PRIOR FILING DATE: 2003-11-24

Query Match 100.0%; Score 14; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUACUUAUUCG 14  
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Db 1 AUAUACUUAUUCG 14

RESULT 13  
US-10-863-973-1829  
; Sequence 1829, Application US/10863973  
; Publication No. US2005014333A1  
; GENERAL INFORMATION:  
; APPLICANT: Richards, Ivan  
; APPLICANT: Polisky, Barry  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Interleukin and  
; TITLE OF INVENTION: Interleukin Receptor Gene Expression Using Short Interfering  
; FILE REFERENCE: 400/163 (MHBB03-084-D)  
; CURRENT FILING DATE: 2004-06-09  
; PRIOR APPLICATION NUMBER: US/10/863,973  
; PRIOR FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: PCT/US03/04566  
; PRIOR FILING DATE: 2004-05-24  
; PRIOR APPLICATION NUMBER: US 10/826,966  
; PRIOR FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US 10/757,803  
; PRIOR FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US 10/720,448  
; PRIOR FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: US 10/693,059  
; PRIOR FILING DATE: 2003-10-23  
; PRIOR APPLICATION NUMBER: US 10/444,853  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: PCT/US03/05346  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: PCT/US03/05028  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1832  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1829  
; LENGTH: 14  
; TYPE: RNA

US-10-861-060-371  
; Sequence 371, Application US/10861060  
; Publication No. US20050137155A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: McSwiggen, James  
; APPLICANT: Haerberli, Peter  
; APPLICANT: Chowhira, Bharat  
; TITLE OF INVENTION: RNA Interference Mediated Treatment of Parkinson Disease Using  
; TITLE OF INVENTION: Short Interfering Nucleic Acid (siNA)  
; FILE REFERENCE: 400/162 (MHBB04-372-A)  
; CURRENT FILING DATE: 2004-06-03  
; PRIOR APPLICATION NUMBER: US/10/861,060  
; PRIOR FILING DATE: 2003-10-31  
; PRIOR APPLICATION NUMBER: US 10/698,311  
; PRIOR FILING DATE: 2003-10-31  
; PRIOR APPLICATION NUMBER: US 10/826,966  
; PRIOR FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US 10/757,803  
; PRIOR FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US 10/720,448  
; PRIOR FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: US 10/693,059  
; PRIOR FILING DATE: 2003-10-23  
; PRIOR APPLICATION NUMBER: US 10/444,853  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: PCT/US03/05346  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: PCT/US03/05028  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1832  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1829  
; LENGTH: 14  
; TYPE: RNA

Query Match 100.0%; Score 14; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUACUUAUUCG 14  
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Db 1 AUAUACUUAUUCG 14

RESULT 13  
US-10-863-973-1829  
; Sequence 1829, Application US/10863973  
; Publication No. US2005014333A1  
; GENERAL INFORMATION:  
; APPLICANT: Richards, Ivan  
; APPLICANT: Polisky, Barry  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Interleukin and  
; TITLE OF INVENTION: Interleukin Receptor Gene Expression Using Short Interfering  
; FILE REFERENCE: 400/163 (MHBB03-084-D)  
; CURRENT FILING DATE: 2004-06-09  
; PRIOR APPLICATION NUMBER: US/10/863,973  
; PRIOR FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: PCT/US03/04566  
; PRIOR FILING DATE: 2004-05-24  
; PRIOR APPLICATION NUMBER: US 10/826,966  
; PRIOR FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US 10/757,803  
; PRIOR FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US 10/720,448  
; PRIOR FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: US 10/693,059  
; PRIOR FILING DATE: 2003-10-23  
; PRIOR APPLICATION NUMBER: US 10/444,853  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: PCT/US03/05346  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: PCT/US03/05028  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1832  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1829  
; LENGTH: 14  
; TYPE: RNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-863-973-1829
  Query Match      100.0%; Score 14; DB 10; Length 14;
  Best Local Similarity 100.0%; Pred. No. 6.5e+03;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUAUAUCUAUUUCG 14
    |||||
Db 1 AUAUAUCUAUUUCG 14

RESULT 14
US-10-922-544-471
; Sequence 471, Application US/10922544
; Publication No. US20050153915A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Early Growth Response
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/204 (MHB03-939-B)
; CURRENT APPLICATION NUMBER: US/10/922,544
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US 60/512,701
; PRIOR FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 471
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-922-544-471

  Query Match      100.0%; Score 14; DB 10; Length 14;
  Best Local Similarity 100.0%; Pred. No. 6.5e+03;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUAUAUCUAUUUCG 14
    |||||
Db 1 AUAUAUCUAUUUCG 14

RESULT 15
US-10-923-330-765
; Sequence 765, Application US/10923330
; Publication No. US20050153916A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
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; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 400/209 (MHB02-708-C)
; CURRENT APPLICATION NUMBER: US/10/923,330
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 765
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-923-330-765

  Query Match      100.0%; Score 14; DB 10; Length 14;
  Best Local Similarity 100.0%; Pred. No. 6.5e+03;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUAUAUCUAUUUCG 14
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Db 1 AUAUAUCUAUUUCG 14

Search completed: June 28, 2006, 23:45:30
Job time : 819 secs
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic ; nucleic search, using sw model

Run on: June 28, 2006, 23:31:55 ; Search time 78 Seconds  
(without alignment)  
212.243 Million cell updates/sec

Title: US-10-824-036A-3578  
Perfect score: 14  
Sequence: 1 auaaucauuuucg 14

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 809770 seqs, 591248006 residues  
Total number of hits satisfying chosen parameters: 454956

Minimum DB seq length: 0  
(Maximum-DB-seq-length:-40)

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq:  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq:  
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7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq:  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12.4	88.6	25	7	US-11-217-529-101087 Sequence 101087,
C 2	12.4	88.6	25	7	US-11-217-529-114875 Sequence 114875,
C 3	11.4	81.4	25	7	US-11-217-529-84996 Sequence 84996, A
4	11.4	81.4	25	7	US-11-217-529-92520 Sequence 92520, A
5	11	78.6	25	7	US-11-217-529-55741 Sequence 55741, A
6	11	78.6	25	7	US-11-217-529-159959 Sequence 159959, A
7	10.8	77.1	25	7	US-11-217-529-49309 Sequence 49309, A
8	10.8	77.1	25	7	US-11-217-529-49452 Sequence 49452, A
9	10.8	77.1	25	7	US-11-217-529-64003 Sequence 64003, A
10	10.8	77.1	25	7	US-11-217-529-64755 Sequence 64755, A
11	10.8	77.1	25	7	US-11-217-529-99687 Sequence 99687, A
12	10.8	77.1	25	7	US-11-217-529-137664 Sequence 137664, A
13	10.8	77.1	25	7	US-11-217-529-166214 Sequence 166214, A
14	10.8	77.1	25	7	US-11-217-529-166369 Sequence 166369, A
15	10.8	77.1	25	7	US-11-217-529-169973 Sequence 169973, A
C 16	10.4	74.3	19	6	US-10-424-339-1385 Sequence 1385, Ap
C 17	10.4	74.3	19	6	US-10-424-339-1566 Sequence 1566, Ap
18	10.4	74.3	19	7	US-11-254-792-2 Sequence 2, Appli
19	10.4	74.3	19	7	US-11-254-792-4 Sequence 4, Appli
C 20	10.4	74.3	25	7	US-11-217-529-7732 Sequence 7732, Ap
21	10.4	74.3	25	7	US-11-217-529-21009 Sequence 21009, A
22	10.4	74.3	25	7	US-11-217-529-28746 Sequence 28746, A
23	10.4	74.3	25	7	US-11-217-529-37826 Sequence 37826, A
24	10.4	74.3	25	7	US-11-217-529-115068 Sequence 115068, A
25	10.4	74.3	25	7	US-11-217-529-131643 Sequence 131643, A

26	10.4	74.3	25	7	US-11-217-529-152354 Sequence 152354,
27	10.4	74.3	25	7	US-11-217-529-166236 Sequence 166236,
28	10.4	74.3	25	7	US-11-217-529-169553 Sequence 169553,
29	10.4	74.3	25	7	US-11-217-529-169560 Sequence 169560,
30	10.4	74.3	25	7	US-11-217-529-172575 Sequence 172575,
31	10.4	74.3	25	7	US-11-217-529-177198 Sequence 177198,
32	10.4	74.3	25	7	US-11-217-529-177654 Sequence 177654,
33	10.4	74.3	25	7	US-11-217-529-184630 Sequence 184630,
34	10.4	74.3	25	7	US-11-217-529-184635 Sequence 184635,
35	10	71.4	25	7	US-11-217-529-86582 Sequence 86582, A
36	10	71.4	25	7	US-11-217-529-99532 Sequence 99532, A
37	10	71.4	25	7	US-11-217-529-105976 Sequence 105976,
38	10	71.4	25	7	US-11-217-529-112907 Sequence 112907,
39	10	71.4	25	7	US-11-217-529-117458 Sequence 117458,
40	10	71.4	25	7	US-11-217-529-150756 Sequence 150756,
C 41	10	71.4	25	7	US-11-217-529-166399 Sequence 166399,
42	10	71.4	25	7	US-11-217-529-171207 Sequence 171207,
43	10	71.4	25	7	US-11-217-529-189684 Sequence 189684,
44	9.8	70.0	24	6	US-10-415-326-15 Sequence 15, Appl
45	9.8	70.0	24	7	US-11-257-502-40 Sequence 40, Appl

## ALIGNMENTS

RESULT 1  
US-11-217-529-101087  
; Sequence 101087, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 101087  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-101087

Query Match 88.6%; Score 12.4; DB 7; Length 25;  
Best Local Similarity 42.9%; Pred. No. 1e+03;  
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AJAAUUAUUCG 14  
DB 2 ATTATCTATTTCG 15

RESULT 2  
US-11-217-529-114875/c  
; Sequence 114875, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529

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; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 114875
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-114875

Query Match      88.6%; Score 12.4; DB 7; Length 25;
Best Local Similarity 42.9%; Pred. No. 1e+03;
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUACUUAUUCG 14
Db 22 ATATATCTATTTC 9

RESULT 3
US-11-217-529-84996/c
; Sequence 84996, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 84996
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-84996

Query Match      81.4%; Score 11.4; DB 7; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.3e+03;
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUACUUAUUC 13
Db 25 ATATATATATTTC 13

RESULT 4
US-11-217-529-92520
; Sequence 92520, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
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; SEQ ID NO 92520
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-92520

Query Match      81.4%; Score 11.4; DB 7; Length 25;
Best Local Similarity 46.2%; Pred. No. 3.3e+03;
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 UAUACUUAUUCG 14
Db 3 TATACTATTTCG 15

RESULT 5
US-11-217-529-55741
; Sequence 55741, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55741
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-55741

Query Match      78.6%; Score 11; DB 7; Length 25;
Best Local Similarity 36.4%; Pred. No. 5.4e+03;
Matches 4; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 2 UAUACUUAUUU 12
Db 14 TATATCTATTTC 24

RESULT 6
US-11-217-529-159959
; Sequence 159959, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 159959
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-159959
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us-10-824-036a-3578.sz40.rnpbn

Thu Jun 29 15:49:22 2006

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Query Match      78.6%; Score 11; DB 7; Length 25;
Best Local Similarity 45.5%; Pred. No. 5.4e+03;
Matches 5; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      3 AUAUACUUAUUCG 13
       |:|:|:|:|:|
Db      2 ATATCTATTTC 12

RESULT 7
US-11-217-529-49309
; Sequence 49309, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49309
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-49309

Query Match      77.1%; Score 10.8; DB 7; Length 25;
Best Local Similarity 42.9%; Pred. No. 6.8e+03;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY      1 AUAUACUUAUUCG 14
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Db      10 ATATATCTCTCTCG 23

RESULT 8
US-11-217-529-49452
; Sequence 49452, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49452
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-49452

Query Match      77.1%; Score 10.8; DB 7; Length 25;
Best Local Similarity 35.7%; Pred. No. 6.8e+03;
Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY      1 AUAUACUUAUUCG 14
       |:|:|:|:|:|
Db      3 ATATATCTTTTTC 16

RESULT 9
US-11-217-529-64003
; Sequence 64003, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 64003
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-64003

Query Match      77.1%; Score 10.8; DB 7; Length 25;
Best Local Similarity 42.9%; Pred. No. 6.8e+03;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY      1 AUAUACUUAUUCG 14
       |:|:|:|:|:|
Db      9 ATATATCTTTTTCG 22

RESULT 10
US-11-217-529-64755
; Sequence 64755, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 64755
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-64755

Query Match      77.1%; Score 10.8; DB 7; Length 25;
Best Local Similarity 35.7%; Pred. No. 6.8e+03;
Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY      1 AUAUACUUAUUCG 14
       |:|:|:~|:|:|
Db      3 ATATATCTTTTTCG 16

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```

; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 169973
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-169973

Query Match      77.1%; Score 10.8; DB 7; Length 25;
Best Local Similarity 50.0%; Pred. No. 6.8e+03;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      1 AUUAUUGUUAUUGG 14
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Db       2 ATATTAATCTTCTG 15

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Job time : 79 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
183.085 Million cell updates/sec

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Perfect score: 14  
Sequence: 1 aaaucauauucy 14

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 115878

Minimum DB seq length: 0  
Maximum DB-seq length: 40

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: gb\_est1.\*  
2: gb\_est3.\*  
3: gb\_est4.\*  
4: gb\_est5.\*  
5: gb\_est6.\*  
6: gb\_hrc.\*  
7: gb\_est2.\*  
8: gb\_est7.\*  
9: gb\_est8.\*  
10: gb\_est9.\*  
11: gb\_gss1.\*  
12: gb\_gss2.\*  
13: gb\_gss3.\*  
14: gb\_gss4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	11.4	81.4	31	14	CT011025	CT011025 KBrH118M0
8	11.4	81.4	32	14	ATH520505	ATH520505 Arabidops
9	11.4	81.4	33	14	BX946340	BX946340 Arabidops
10	11.4	81.4	34	14	DR61F19S	AL982633 Danio rer
11	11	78.6	32	11	A1587460	A1587460 tr51a02.x
12	11	78.6	32	11	BH847194	BH847194 SALK_0445
13	11	78.6	38	12	CC793445	CC793445 SALK_0143
14	10.8	77.1	24	11	BH853216	BH853216 SALK_0761
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16	10.8	77.1	38	11	BH810085	BH810085 SALK_0406
17	10.8	77.1	39	11	AU264278	AU264278 AU264278
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21	10.4	74.3	21	11	AZ375571	AZ375571 1M0129B05
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23	10.4	74.3	25	1	AI761999	AI761999 wH50909.x
24	10.4	74.3	25	11	AZ371135	AZ371135 1M0122N04
25	10.4	74.3	25	11	AZ625569	AZ625569 1M0465112
26	10.4	74.3	25	14	ATH528692	AJ528692 Arabidops
27	10.4	74.3	25	14	ATH528882	AJ528882 Arabidops
28	10.4	74.3	27	5	CD576920	CD576920 2L_B03.21
29	10.4	74.3	27	11	BZ353129	BZ353129 SALK_1198
30	10.4	74.3	27	14	TA175807Q	AL475337 T. brucei
31	10.4	74.3	28	11	AZ786457	AZ786457 2M0032B03
32	10.4	74.3	29	11	AZ796712	AZ796712 2M0052M03
33	10.4	74.3	29	13	CZ486260	CZ486260 f03682-5p
34	10.4	74.3	30	11	AZ366827	AZ366827 1M0116B17
35	10.4	74.3	30	13	CZ484387	CZ484387 f01890-3p
36	10.4	74.3	31	11	BH853786	BH853786 SALK_0782
37	10.4	74.3	31	14	BX532321	BX532321 Arabidops
38	10.4	74.3	31	14	BX532876	BX532876 Arabidops
39	10.4	74.3	31	14	BX949761	BX949761 Arabidops
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42	10.4	74.3	32	13	CL658452	CL658452 PRI0131C-
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45	10.4	74.3	33	14	TA82C08P	AL462241 T. brucei

ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION  
ywc3h05.sl Soares placenta 8to9weeks 2NbHP8to9W Homo sapiens cDNA  
clone IMAGE:256953.3 similar to gb:L03558 CYSTATIN B  
(HUMAN); contains Alu repetitive element;; mRNA sequence.

ACCESSION  
N30120  
VERSION  
N30120.1 GI:1148640  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE  
1 (bases 1 to 34)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Ma, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

TITLE  
The WashU-Merck EST Project  
JOURNAL  
Unpublished (1995)  
COMMENT  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 4  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: ml3 -40 forward  
High quality sequence stop: 4.  
Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="GDB:3886563"  
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/dev\_stage="two placentae: one from 8 weeks and another

from 9 weeks post conception"  
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/clone\_lib="Soares placenta\_8to9weeks\_2NBP8to9W"  
/notes="Organ: placenta; Vector: pT7T3D (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCGAAGTGGGCGGCGGATTTTTTTTTTTT 3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector  
(Pharmacia). Library constructed by Bento Soares and  
M.Fatima Bonaldo."

ORIGIN

Query Match 88.6%; Score 12.4; DB 10; Length 34;  
Best Local Similarity 42.9%; Pred. No. 8.7e+04;  
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUUAUCUAUUUCG 14  
Db 12 ATATATCTATTTCG 25

RESULT 2  
LOCUS BZ291752/c 36 bp DNA linear GSS 24-OCT-2002  
DEFINITION SALK\_121715.40.90.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_121715.40.90.x, genomic  
survey sequence.

ACCESSION BZ291752  
VERSION BZ291752.1 GI:24337754  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 36)  
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
JOURNAL Unpublished (2001)  
COMMENT Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA. This sequence lies within 300 bases of the 3' end of  
At2g18700 and 300 bases of the 3' end of At2g18710.  
Class: TDNA tagged.  
Location/Qualifiers  
1. .36  
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/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/notes="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

FEATURES

source  
Query Match 85.7%; Score 12; DB 11; Length 36;  
Best Local Similarity 41.7%; Pred. No. 1.4e+05;  
Matches 7; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

Query Match 85.7%; Score 12; DB 11; Length 36;  
Best Local Similarity 41.7%; Pred. No. 1.4e+05;  
Matches 7; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
QY 2 UAUAUCUAUUUC 13  
Db 24 TATATCTATTTC 13

RESULT 3  
LOCUS BZ291754/c 36 bp DNA linear GSS 24-OCT-2002  
DEFINITION SALK\_121717.36.85.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_121717.36.85.x, genomic  
survey sequence.

ACCESSION BZ291754  
VERSION BZ291754.1 GI:24337762  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 36)  
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
JOURNAL Unpublished (2001)  
COMMENT Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA. This sequence lies within 300 bases of the 3' end of  
At2g18700 and 300 bases of the 3' end of At2g18710.  
Class: TDNA tagged.  
Location/Qualifiers  
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/notes="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

FEATURES

source  
Query Match 85.7%; Score 12; DB 11; Length 36;  
Best Local Similarity 41.7%; Pred. No. 1.4e+05;  
Matches 5; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

Query Match 85.7%; Score 12; DB 11; Length 36;  
Best Local Similarity 41.7%; Pred. No. 1.4e+05;  
Matches 5; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 2 UAUAUCUAUUUC 13  
Db 24 TATATCTATTTC 13

RESULT 4  
LOCUS AZ958303/c 20 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0225106R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0225106 R, genomic survey sequence.

ACCESSION AZ958303  
VERSION AZ958303.1 GI:13829930  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

**ORGANISM**  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridea; Muridae; Murinae; Mus.  
**REFERENCE**  
 1 (bases 1 to 20)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Iqbal, H., Longacre, S., Mamoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weis, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
**JOURNAL**  
 Unpublished (2000)  
**COMMENT**  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0225 row: 1 column: 06  
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 High quality sequence stop: 20.  
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 /db\_xref="taxon:10090"  
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 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGC2M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (female) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

**KEYWORDS**  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.  
**REFERENCE**  
 1 (bases 1 to 25)  
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
**JOURNAL**  
 Unpublished (1997)  
**COMMENT**  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapsb@mail.nih.gov  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Trace considered overall poor quality  
 Insert Length: 418 Std Error: 0.00  
 Seq primer: -40ml3 fwd. ET from Amersham  
 High quality sequence stop: 1.  
**FEATURES**  
 source  
 1..25  
 /location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1682088"  
 /tissue\_type="senescent fibroblast"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares senescent fibroblasts NBHSF"  
 /note="Vector: pT7T3D (Pharmacia) with a modified  
 polylinker V-TYPE; phagemid; Site 1: Not I; Site 2: Eco  
 RI; 1st strand cDNA was primed with a Not I - oligo(dT)  
 primer [5'  
 TGTACCAATCTGAAGTCGAGCGCCGCAATTTTTTTTTTTTTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT7T3 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 81.4%; Score 11.4; DB 1; Length 25;  
 Best Local Similarity 46.2%; Pred. No. 2.8e+05;  
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
**Qy**  
 1 AUAUAUCUAUUUC 13  
 |::|::|::|  
**Db**  
 20 ATATATCTATTC 8  
**RESULT 6**  
 BX946341/c  
**LOCUS**  
 Arabidopsis thaliana T-DNA flanking sequence GK-761A05-024641,  
 genomic survey sequence.  
**DEFINITION**  
 BX946341  
 BX946341.1 GI:42596027  
 GSS.  
**KEYWORDS**  
 Arabidopsis thaliana (thale cress)  
**SOURCE**  
 ORGANISM  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
**REFERENCE**  
 1  
 Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weishaar, B.  
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for  
 the identification of T-DNA insertion mutants in Arabidopsis  
 thaliana  
 Bioinformatics 19 (11), 1441-1442 (2003)  
 12874060  
**JOURNAL**  
 PUBLISHED  
**REFERENCE**  
 2  
 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and  
 Weishaar, B.

**TITLE**  
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse Genetics  
**JOURNAL**  
Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
**REFERENCE**  
14756321

**AUTHORS**  
Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weishaar, B.

**TITLE**  
High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines  
**JOURNAL**  
Biotechniques 35 (6), 1164-1168 (2003)  
**REFERENCE**  
14682050

**AUTHORS**  
Li, Y., Strizhov, N., Rosso, M.G. and Weishaar, B.

**TITLE**  
Direct Submission  
**JOURNAL**  
Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
**COMMENT**  
This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone F24B18. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpi-z-koeln.mpg.de/GABI-Kat/>.

**FEATURES**  
source  
Location/Qualifiers  
1..30  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="GK-761A05-024641"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Col-0"  
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

**ORIGIN**  
Query Match 81.4%; Score 11.4; DB 14; Length 30;  
Best Local Similarity 38.5%; Pred. No. 2.8e+05;  
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

**Qy** 1 AUAUACUUAUUC 13  
|:|:|:|:|:|  
**Db** 21 ATATATATATTC 9

**RESULT 7**  
**CT011025** 31 bp DNA linear GSS 09-AUG-2005  
**LOCUS** KBrH18M09 genomic clone, KBrH (HindIII) BAC library Brassica rapa subsp. pekinensis, genomic survey sequence.  
**DEFINITION**  
**ACCESSION** CT011025  
**VERSION** CT011025.1 GI:71479066  
**KEYWORDS** GSS.  
**SOURCE** Brassica rapa subsp. pekinensis  
**ORGANISM** Brassica rapa subsp. pekinensis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; euroside II; Brassicales; Brassicaceae; Brassica.

**REFERENCE**  
1. Viehoveer, P., Holtgraewe, D. and Weishaar, B.  
**AUTHORS** BAC end sequences of Brassica rapa  
**TITLE** Unpublished  
**JOURNAL** 2 (bases 1 to 31)  
**REFERENCE** Li, Y. and Weishaar, B.  
**AUTHORS** Direct Submission  
**TITLE** Submitted (09-AUG-2005) Weishaar B., Bielefeld University, Institute for Genome Research, Universitaetsstrasse 25, D-33594 Bielefeld, Germany

**COMMENT**  
Contact: Bernd Weishaar  
Bielefeld University, Institute for Genome Research  
Universitaetsstrasse 25, D-33594 Bielefeld, Germany Email: bernd.weishaar@uni-bielefeld.de  
BAC end sequences of Brassica rapa BAC clone KBrH18M09; generated as contribution to the 'Multinational Brassica rapa Sequencing Project'. Seq primer: sp6B ATTAGGTGACACTATAG  
Class: BAC ends.  
Location/Qualifiers  
1..31  
/organism="Brassica rapa subsp. pekinensis"  
/mol\_type="genomic DNA"  
/strain="Chifu type 401-42"  
/cultivar="Chifu"  
/sub\_species="pekinensis"  
/db\_xref="taxon:51351"  
/clone="KBrH18M09"  
/clone\_lib="KBrH, Brassica rapa HindIII BAC library GF-SCF-1002. Vector: pCUGIBac1"  
/lab\_host="E.coli DH10B"

**FEATURES**  
source  
Location/Qualifiers  
1..31  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Wassilewskija"

**ORIGIN**  
Query Match 81.4%; Score 11.4; DB 14; Length 31;  
Best Local Similarity 38.5%; Pred. No. 2.8e+05;  
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

**Qy** 1 AUAUACUUAUUC 13  
|:|:|:|:|:|  
**Db** 17 ATTTATCTATTC 29

**RESULT 8**  
**ATH520505** 32 bp DNA linear GSS 08-FEB-2006  
**LOCUS** Arabidopsis thaliana T-DNA flanking sequence, left border, clone 036C02, genomic survey sequence.  
**DEFINITION**  
**ACCESSION** AJ520505  
**VERSION** AJ520505.1 GI:26788741  
**KEYWORDS** GSS; left border; T-DNA flanking sequence.  
**SOURCE** Arabidopsis thaliana (thale cress)  
**ORGANISM** Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; euroside II; Brassicales; Brassicaceae; Arabidopsis.

**REFERENCE**  
1. Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.  
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
**JOURNAL** EMBO Rep. 3 (12), 1152-1157 (2002)  
**PUBMED** 12446565  
**REFERENCE** 2 (bases 1 to 32)  
**AUTHORS** Balzergue, S.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publicines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

**FEATURES**  
source  
Location/Qualifiers  
1..32  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Wassilewskija"



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/db xref="taxon:3702"
/clone="036C02"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
1. .32
misc_feature
/notes="T-DNA flanking sequence
left border"

ORIGIN
Query Match      81.4%; Score 11.4; DB 14; Length 32;
Best Local Similarity 38.5%; Pred. No. 2.8e+05;
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUAUCUAUUC 13
|:|:|:|:|:|
Db 13 ATATATCTTTTC 25

RESULT 9
BX946340/c
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence GK-761A05-024593,
genomic survey sequence.
ACCESSION
BX946340
VERSION
BX946340.1 GI:42596026
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 Li.Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
GABI-Kat Simplesearch: a flanking sequence tag (fST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
12874060
2
Rosso,M.G., Li.Y., Strizhov,N., Reis,B., Dekker,K. and
Weisshaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
14756321
3
Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and
Weisshaar,B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
14682050
4 (bases 1 to 33)
Li.Y., Strizhov,N., Rosso,M.G. and Weisshaar,B.
Direct Submission
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
F24818. Details on the protocols used for generation of the
sequence are described in References 1-3. The sequences are
generated at the MPI for Plant Breeding Research in the context of
the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
program designated 'GABI'. Information on line availability can be
found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
1. .33
/organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"

FEATURES
source

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/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN
Query Match      81.4%; Score 11.4; DB 14; Length 33;
Best Local Similarity 38.5%; Pred. No. 2.8e+05;
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUAUCUAUUC 13
|:|:|:|:|:|
Db 24 ATATATATATTC 12

RESULT 10
DR61F19S/c
LOCUS
DEFINITION
Danio rerio genomic clone DKEY-61F19, genomic survey sequence.
ACCESSION
AL982633
VERSION
AL982633.1 GI:25187375
KEYWORDS
GSS.
SOURCE
Danio rerio (zebrafish)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 34)
Humphray,S.J., Huckle,E. and Hunt,S.E.
Direct Submission
Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquerry@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 61F19. 61F19 is
part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene.
Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
1. .34
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-61F19"
/tissue_type="Testis"
/note="Vector pIndigoBAC-536"

FEATURES
source
Query Match      81.4%; Score 11.4; DB 14; Length 34;
Best Local Similarity 46.2%; Pred. No. 2.8e+05;
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUAUCUAUUC 13
|:|:|:|:|:|
Db 29 ATATATCTATATC 17

RESULT 11
AI587460
LOCUS
DEFINITION
t551402.x1 NCI CGAP Panel Homo sapiens cDNA clone IMAGE:2221802 3',
similar to gb|U10284 CALNEXIN PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION
AI587460
VERSION
AI587460.1 GI:4573901
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 32)

```

**AUTHORS** NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
**JOURNAL** Unpublished (1997)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
Email: [CGAPs@mail.nih.gov](mailto:CGAPs@mail.nih.gov)  
Life Technologies catalog #: 11548-013  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
Insert length: 636 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1  
POLYA=No.

**FEATURES** Location/Qualifiers  
source  
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/clone="IMAGE:2221802"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B"  
/clone\_lib="NCI-CGAP\_Pan1"  
/notes="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"

**ORIGIN**  
Query Match 78.6%; Score 11; DB 1; Length 32;  
Best Local Similarity 36.4%; Pred. No. 4.4e+05;  
Matches 4; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 UAUUUCUUAUU 12  
|:|:|:|:|:|:  
Db 1 TATATCTATT 11

**RESULT 12** BH847194 32 bp DNA linear GSS 13-JUN-2002  
**LOCUS** SALK\_044576.45.35.x Arabidopsis thaliana TDNA insertion lines  
**DEFINITION** Arabidopsis thaliana genomic clone SALK\_044576.45.35.x, genomic survey sequence.

**ACCESSION** BH847194  
**VERSION** BH847194.1 GI:21418065  
**KEYWORDS** GSS.  
**SOURCE** Arabidopsis thaliana (thale cress)  
**ORGANISM** Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

**REFERENCE** 1 (bases 1 to 32)  
**AUTHORS** Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
Shinn,P., Zimmerman,J. and Ecker,J.R.  
**TITLE** A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
**JOURNAL** Unpublished (2001)  
**COMMENT** Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: [ecker@salk.edu](mailto:ecker@salk.edu)  
This is single pass sequence recovered from the left border of  
TDNA.  
Class: TDNA tagged.  
Location/Qualifiers

**FEATURES** source  
Query Match 78.6%; Score 11; DB 12; Length 38;  
Best Local Similarity 45.5%; Pred. No. 4.4e+05;

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/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/notes="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

**ORIGIN**  
Query Match 78.6%; Score 11; DB 11; Length 32;  
Best Local Similarity 45.5%; Pred. No. 4.4e+05;  
Matches 5; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AUAUUCUUAUU 11  
|:|:|:|:|:|:  
Db 22 ATATATCTATT 12

**RESULT 13** CC793445 38 bp DNA linear GSS 01-JUL-2003  
**LOCUS** SALK\_014384.21.55.n Arabidopsis thaliana TDNA insertion lines  
**DEFINITION** Arabidopsis thaliana genomic clone SALK\_014384.21.55.n, genomic survey sequence.

**ACCESSION** CC793445  
**VERSION** CC793445.1 GI:32388668  
**KEYWORDS** GSS.  
**SOURCE** Arabidopsis thaliana (thale cress)  
**ORGANISM** Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

**REFERENCE** 1 (bases 1 to 38)  
**AUTHORS** Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
Shinn,P., Zimmerman,J. and Ecker,J.R.  
**TITLE** A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
**JOURNAL** Unpublished (2001)  
**COMMENT** Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: [ecker@salk.edu](mailto:ecker@salk.edu)  
This is single pass sequence recovered from the left border of  
TDNA.  
Class: TDNA tagged.  
Location/Qualifiers

**FEATURES** source  
1..38  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone="SALK\_014384.21.55.n"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/notes="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

**ORIGIN**  
Query Match 78.6%; Score 11; DB 12; Length 38;  
Best Local Similarity 45.5%; Pred. No. 4.4e+05;

Matches 5; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUCUAUU 11  
|:|:|:|:|:  
Db 27 ATATATCTATT 37

RESULT 14  
BH853216  
LOCUS 24 bp DNA linear GSS 13-JUN-2002  
DEFINITION SALK\_076188.27.55.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_076188.27.55.x. genomic  
survey sequence.

ACCESSION BH853216  
VERSION BH853216.1 GI:21424087  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 24)  
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
Gadrinab, C., Jekker, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
Shinn, P., Zimmerman, J., and Ecker, J.R.  
TITLE A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
JOURNAL Unpublished (2001)  
COMMENT Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA. This sequence lies within an annotated exon of At5g10720.  
Class: TDNA tagged  
Location/Qualifiers  
1..24  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
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/clone="SALK\_076188.27.55.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/notes="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

ORIGIN  
Query Match 77.1%; Score 10.8; DB 11; Length 24;  
Best Local Similarity 50.0%; Pred. No. 5.6e+05;  
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 AUAUAUCUAUUUCG 14  
|:|:|:|:|:  
Db 1 ATATATCTACTCG 14

RESULT 15  
A2789033  
LOCUS 25 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0036H02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0036H02 R. Genomic survey sequence.

ACCESSION A2789033  
VERSION A2789033.1 GI:12929432  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 25)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A., and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0036 row: H column: 02  
Seq primer: CACACAGGAACACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 25.  
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/sex="Male"  
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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (GI:4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN  
Query Match 77.1%; Score 10.8; DB 11; Length 25;  
Best Local Similarity 35.7%; Pred. No. 5.6e+05;  
Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 AUAUAUCUAUUUCG 14  
|:|:|:|:|:  
Db 4 ATATATATATTGG 17

Search completed: June 29, 2006, 00:51:16  
Job time : 4277 secs

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